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-MODEL=frame+ p2n.model -DEV=xlh
-Q=/CgD1_J/USPTO_spool/US09657631/runat_10082004_171045_1674/app_query.fasta_1.1294
-Q=/CgD2_J/USPTO_spool/US09657631/runat_10082004_171045_1674/app_query.fasta_1.1294
-Q=/CgD2_J/USPTO_spool/US09657631/runat_10082004_171045_1674/app_query.fasta_1.1294
-UNITS=bits -GTART=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-UNITS=bits -GTRAT=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-UNITS=bits -GTRAT=1 -END=-1 - MATRIX=500 - TRR MAX=0 - ALRA MAXLEN=200000000
-USRS=US0657631_GCGN 1 1 6617_@runat_10082004_171045_1674_-NCPU=6 -ICPU=3
-NO MMAP-LARGEQUER* -NGG_CORRES=0 - MAIT -DSPEDGCK=100 -JONGIAG
-DBV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
                                                             August 19, 2004, 13:58:01; Search time 5578.11 Seconds (without alignments) 3589.832 Million cell updates/sec
                                                                                                      US-09-657-631-2
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1 MNWVWPKTKSMSFLLLITFL......GTALEAISSLPKFNRLMYFI 462
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                        - nucleic search, using frame_plus_p2n model
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                             GlySerSerGlySerArgValHisValPheAsnPheAspGlnAsnLeuAspLeuLeuHis
                                                          230 GGTAGCTCTGGGAGTCGTGTCCATGTCTTCAATTTTGACCAGAACTTAGATCTCCTGCAC
                                                                                       IleGlyAsnAspleuGluPheThrLysLysIleLysProGlyLeuSerTyrAlaAsp
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Bukaryota; Varidiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota; Varidiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Dolichos:
1 (bases: 1 to 1608)
Etzler,M.E., Kalsi,G., Ewing,N.N., Roberts,N.J., Day,R.B. and
Murphy,U.B.
A nod factor binding lectin with apyrase activity from legume roots
Proce. Natl. Acad. Sci. U.S.A. 96 (10), 5856-5861 (1999)
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IFFARTSTAVIFDAGSSGRYVHYNFDQNILDLHGUNDLEFFKKITGSLSSYDKP
IRPOGELITSTAVIFDAGSSGRYVHYNFDQNILDLHGUNDLEFFKKITGSLSSYDKP
IRPOGELITSTAVI IDED BODVPPELHPKTPLKLGATAGIR LLDGDAAEKTLLQAVEBRRNR
SSLSVQPDAVSVIDGGOGSYLWYTVNYLLGKLGKKFTKTVGVIDLGGASVQMATAVS
RYTRAKAPROPGEDPYMKKVJVLGKKYDLYNFSTRYTGVGASVQMATAVS
ILLAGYEDIXYS GGSYNIYQFTSGANFNECRDLALQTLALNFPCSHRNCTFGGIWDGG
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CA 95616, USA
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Etzler,M.E., Kalsi,G., Ewing,N.N., Roberts,N.J., Day,R.B.
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phosphohydrolase"
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                                                                                                                                                                                                                                                                                                                                                       Submitted (31-MAR-1999) Molecular and Cellular of California, Davis, 1 Shields Avenue, Davis, Location/Qualifiers
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Mismatches:
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50. .1438
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Direct Submission
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10318974
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AUTHORS
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SOURCE Unknown. ORGANISM Unknown. Unclassified.	CE 1 (bases 1 to 6265) RS Etzler, M.E. and Murphy, J.B.	ы	FEATURES LOCATION/QUALITIES SOURCE 16265	/organism="unknown" /mol_type="genomic DNA" ORIGIN	Length:	1741.00 Matches: 29.01% Conservative:	t Local Similarity: 29.01% Mismatches: ry Match: 72.42% Indels:	sdab 9.	US-U9-65/-631-Z (1-462)	AIGHTHILL AIGECCAAAGACAAAGAGAIGAGCTICCTACICCICAICACTITIC	Cy 21 LeuPheSerLeuProLysLeuSerSerGlnTyrValGlyAsnSerIleLeuLeuAsn 40	Db 735 CICTICICATIGCCAAAACITICITCTICGCAATATGTIGGGAACAGTATCTIACTAAAT 794	HisArgLysIleLeuProAsnGlnGluLeuLeuThrSerTyrAlaValIlePheAspAla	795 CATCGTAAGATACTTCCCAACCAGGAACTCCTTAACCTCTTACGCTGTCATCTTTGATGCT	19	GGIAGCICIGGGAGICGIGICCAIGICIICAAIIITGACCAGAACIIAGAICICCIGCAC	81 IleGlyAsnAspLeuGluPheThrLyBlys	V. [Octobrile] V. [Ottobrile] I. [Ottobrile] V. [Ot	ATTTCTTCATCTTACTTACATTCTTCTTATTCTGGTGCAGATCAAAGCCGGT	euLeuGlu	TGCAGAATCTCTCATTCCACTTTTGGAG	115 GluAlaGluAspValValProGluGluLeuHisProLysThrProLeuLysLeuGly	5 GAGGCIGAAGAIGTIGTCCCIGAGGAACIGCACCCCAAGACACCCCIIAAGCIIGGGGIG	133	5 AGIALLICICALCIACILLIGGCACAGALIMAIAIGI CACACLILLIMCALGAMANCAGA	13.3		Db 1275 CTAGAACTTAAACTATGGTAATATAAAATGAATATGAAACTAATATATAT	Ογ 133 133	Db 1335 ACAGAAGAAAGAATAICAAGAGAGAGACAAAACACACACTTTGATGAGCTCTATCTTTTAA 1394	Qy 133 133

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δλ	184 184	δλ	251 251
qq	2714 AATATTTATAATATATATAATTTAAATTTCAAACTTGTGATGTTACTTATAAATTA 2773	ପ୍ଧ	3794 AATCAGTCTTCATAAATAGTATTTATGTAGATCCAAATAGAGGCTTAACGTGGTCTAGTT 3853
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qq	2774 AFTATTTTTTCAGTTTTCAATTATTGCATTTTTCTTATAATATTCACTATATAATATT 2833	qq	3854 GTACAAACCTAAAAGGTGTTTCTTTTTTTTTTTAATTTGAAGAACTAGAATATTGTTTTT 3913
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DÞ	2834 TGACAATATTTCAAAACATTTTCAATAAAAAAAAAAAAA	qq	3914 CAAITIGAAAGACGAAGGCAAACITAACCAAAITIAGAAAAAGTAAAAACITGGITAACT 3973
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λō		δλ	251 251
Dp	3134 GTCTCAAGAAATACAGCTAAAAATGCCCCAAAAACCACCACAAGAGAGAG	qq	4214 TITITIAIGGITTAACIGATAAATAIGCAIGAGICAIGICAI
ζ	237 LysLysLeuValLeuLysG]yLysLysTyrAspLeuTyrValHis 251	ð 1	252SerTyrLeuArgTyrGlyAsnAspAlaAlaAlaAlLysIle 265
QD	3194 AAGAAGCTIGTACTCAAGGGAAAGAAATATGACCTTTATGTTCACAGGTTACTTTCTGTT 3253	a i	AAICAACIICIIIGIIGCAGIIACIIGCGIIAIGGIAACGACGACGACGACGIGTIAAGAIT
ò	251 251	Š	266 PhenysThrThrAsp61yAlaAlaAlaSerProCysLeuLeuAlaGJyTyrGlu282
qq	3254 ATCATTCATATAGCAAAGGAACAATTATCATTTCAATTTCTAAAATATATTTATAATCTC 3313	3 8	iirasancacisaissiscisciaciastissistä ja
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qq	3434 ATTGTTTGGATTATTAGAAAGAGAAAAAGTTGAATAATTATT	an .	TGACCAAAGTTACTTTTTCCTCACTGAGTTCTATTGAAATGCAGAAACTTGTTGCAGATA
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		λŏ	283 AspileTyrArgTyrSerGlyGluSerTyrAsnileTyrGlyProThrSerGlyAlaAsn 302

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STYNNARABERLEYQDALVEBABH

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  Denny, R.L., Dunlap, J.
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Day, R. B., McAlvin, C. B., Loh, J. T., Fink, S. E., Denny, R. L., Dunlap, J. Young, N. D. and Stacey, G. Direct Subnission Subnitted (2.1-NOV-1999) Microbiology, The University of Tennessee, M409 Walters Life Science Building, Knoxville, TN 37996-0845, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GlySerSerGlySerArgValHisValPheAsnPheAspGlnAsnLeuAspLeuLeuHis
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Indels:
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Day,R.B., McAlvin,C.B., Loh,J.T., Denny,R.L., Wood,T.C., Young,N.D.
and Stacey,G.
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Unclassified. 1 (bases 1 to 1489) Etzler, M.E. and Murphy, J.B.

Unknown. Unknown

> ORGANISM REFERENCE AUTHORS

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Mismatches:
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Lotus corniculatus var. japonicus
Lotus corniculatus var. japonicus
Sukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Loteae;
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Roberts, N.J., Brigham, J., Wu, B., Murphy, J.B., Volpin, H., Phillips, D.A. and Etzler, M.E.
A Nod factor-binding lectin is a member of a distinct class apyrases that may be unique to the legumes
Mol. Gen. Genet. 262 (2), 261-267 (1999)
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    1489
/organism="Lotus corniculatus var. japonicus"

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Roberts, N.J., Brigham, J., Wu,
Phillips, D.A. and Etzler, M.E.
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                                                                                  Cullimore, J.V. and Niebel, A.
Cullimore, J.V. and Niebel, A.
Direct Submission
Submitted (15-NOV-2002) Laboratoire de Biologie Moleculaire des
Relations Plantes-Microorganismes, INRA-CNRS, Castanet-Tolosan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25 ProLysLeuSerSerSerGlnTyrValGlyAsnSerIleLeuLeuAsnHisArgLysIle
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids I; Fabales, Fabaceae, Papilionoideae, Trifolieae,
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|GCTGGCTTTGATGGGGCATATACATATCCGGAGCAGAGTATAAGGTCTCGGCCCCAGCT
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                                           AAGACAGTGGGAGTTGATCTAGGAGGTGGGTCAGTGCAAATGACATATGCAGTCTCA
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                                                                                                             673 AGGAACACAGCTAAAAATGCTCCAAAAGTACCTGAAGGAGAGGATCCATAAAGAAG
                                                                                                                                                                        AlaGlyTyrGluAspIleTyrArgTyrSerGlyGluSerTyrAsnIleTyrGlyProThr
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|GTAAAACAAATCTTGAGGATGCAAAATCCAAATACCCAGATCTTTATGAGAAAGACAGT
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Navarro-Gochicoa,M.T., Camut,S., Niebel,A. and Cullimore,J.V.
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             AlaAlaGluLysIleLeuGlnAlaValArgGluMetPheArgAsnArgSerSerLeuSer
                     CACCCCAAAACACCCCTTAGGCTTGGGGCAACCGCAGGTTTGAGGCTTTTGAATGGGGAT
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AR237864 Sequence 8 from patent AR237864 AR237864.1 GI:27282687

RESULT 8
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Unclassified.

I (bases 1 to 1458)

RS Etzler,M.E and Murphy,J.B.

Nod factor binding protein from legume roc

NAL Patent: US 6465716-A 8 15-OCT-2002;

Location/Qualifiers

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"...known"
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Matches:
Conservative:
Mismatches:
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
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Submitted (07-UTN-1999) Molecular and Cellular Biology, University
of California, Davis, 1 Shields Avenue, Davis, CA 95616, USA
Location/Qualifiers
                       LysThrThrAspGlyAlaAlaSerProCysLeuLauAlaGlyTyrGluAspIleTyrArg
                                                                                                                                                                                    PheGlyGlyIleTrpAspGlyGlyLysGlySerGlyGlnLysAsnLeuValValThrSer
                                     AATGCAACTAATGGATCTGCTAACCCTTGCATTTTACCTGGATTTAATGGGACCTTTACA
                                                                                           304 AAAGAAATAATTCTTAAAGTTCTTAAAGTAAATGATCCATGTCCCTATCCGAGTTGCACT
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A Nod factor-binding lectin is a member of a distinct class apyrases that may be unique to the legumes
Mol. Gen. Genet. 262 (2), 261-267 (1999)
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Roberts, N.J., Brigham, J., Wu, B., Murphy, J.B., Volpin, H.
Phillips, D.A. and Etzler, M.E.
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LEEREDWUVPEDLHFKTPLRIGATAGIRLINGDAARKILOATRNMESNRSTINVORDA
VZI DGTQEGSYMWTYNYYLGNLGKSFTKSVQVDIDGGGSVQMTYAVSKRTAKNAPK
VADGRDPYIKKLVILKGKQYDLIYHSYLRFGKEATRAQVILNITNGSARPCILLFGFNGTF
TYSGVEYKAFSPSSGSNFDDCKEI ILKVLKVNDPCPYPSCTFGGIWNGGGSGQCKKLF
TYSAFAXLABDVGWVEDNKRSILHPVDFEIEAKRACALNFEDWKSTYPRLTDAKRPY
VCMDLLYQHVLLVHGFGLGFRKEITVGEGQYQNSVVBAAMPLGTAVEAISALPKFKR
                                                                                                                                                                                                                                                                                 translation="MEFLITLIATFLLLLMPAITSSQYLGNNLLTNRKIFQKQETLTS"
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Mismatches:
Indels:
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Matches:
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                                                                                                                                                                                                                  phosphohydrolase'
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/ LTAIRSTALTONS - "WYLLWONTKNINGNTLITELLFIMPSISYSQYLGNNILLTNRK
IFPKQEPISSYAVVEDAGSTGSRVHYYHFDQNLALLHVGKDVEFYNKTTFGLSAJADN
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Cullimore, J.V. and Niebel, 3.
Direct Submission
Submitted (15-NOV-2002) Laboratoire de Biologie Moleculaire des
Relations Plantes-Microorganismes, INRA-CNRS, Castanet-Tolosan
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                                                                                                                                  organism="Medicago truncatula"
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7. .1410
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Plant Physiol. 131 (3), 1124-1136 (2003)
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Spernatophyta; Magnoliophyta; eudicotyledons; core eudicots;
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                                        666 AAAGTTGCTGATGGAGGATCCATATATAAGAAGCTTGTGCTCAAGGGAAAGCAATAT
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                                                                                                                                                                                                                               ArgAspLeuAlaLeuGln1leLeuArgLeuAsnGluProCysSerHisGluAsnCysThr
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                                                                              LysProProGlnGlyGluAspProTyrMetLysLysLeuValLeuLysGlyLysLysTyr
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                                                                                       Navarro-Gochicoa, M.T., Camut, S., Niebel, A. and Cullimore, J.V.
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truncatula Is Induced Rapidly and Transiently by Stress and Not by
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                  truncatula (barrel medic)
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Cullimore, J.V. and Niebel, A.
Direct Submission
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GGGGATGCTTCTGAAAAAAAACTGCAATCGGTAAGGGATTTGTTCAGCAATAGAAGTACC
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                       LeuSerValGlnProAspAlaValSerValIleAspGlyThrGlnGluGlySerTyrLeu
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                                                                        TrpValThrValAsnTyrLeuLeuGlyLysLeuGlyLysLysPheThrLysThrValGly
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1348 TGCATGGCCACTAGGCAATGCTGTAGAAGCCATATCATCGTTACCTAAATTTGAAAAATT 1407
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Direct Submission

Bibmitted (IT-JUL-2000) Microbiology, University of Tennessee, M409

Walters Life Sciences Bldg., Knoxville, TN 37996, USA

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cohn,J.R., Uhm,T., Ramu,S., Nam,Y.W., Kim,D.J., Penmetsa,R.V., Wood,T.C., Denny,R.L., Young,N.D., Cook,D.R. and Stacey,G. Differential regulation of a family of apyrase genes from Medicago
                                                                                                                                                                                                                                                                                                                                               Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                    Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
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                                                                                                                                                                 AF288132 1401 bp mRNA linear
Medicago truncatula putative apyrase (apy1) mRNA,
AF288132
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Conservative:
Mismatches:
Indels:
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Eukaryota, Viridiplantae, Streptophyta;
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/gene="apy1"
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                         381 ThrPheGluGluAlaLysSerThrPheProAsnValGluLysAspLysLeu---ProPhe 399
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Shibata,K., Morita,Y., Abe,S., Stankovic,B. and Davies,E.
Apyrase from pea stems: Isolation, purification, characterization and identification of a NTPase from the cytoskeleton fraction of
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Pisum sativum mRNA for S-type apyras, complete cds, clone:pKS5-1.
ABO27613
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32. 1399
/EC_number="3.6_1.5"
/standard_name="ATP diphosphohydrolase"
/note="ATP diphosphohydrolase"
/citation=[1]
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/mol_type="mRNA"
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GTATGCATGGATCTTATATATACAGTATGTGTTACTCGTTGATGGATTTGGTCTTGATCCA 1267
                                                                                                                                                                                                                                                                                                                                                       TTGCTTCTTCATCTTTACCTACCTGAAGATACCGGTATGGTTGATGCAAGCACA 1087
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Pisum sativum (pea)
Pisum sativum
Bukariayu Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Viridiplantae; Streptophyta; core eudicots; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Vicieae;
                                                                                                                                                                                                                                                                                                                              343 ValValThrSerAlaPheTyrTyrArgSerSerGluValGlyPheVal-----ThrPro 360
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Direct Submission
Submitted (22-FEB-2000) Shunnosuke Abe, Ehime University, College Abgriculture; Tarumi 3-5-7, Matsuyama, Ehime 790-8566, Japan (E-mail:abe@mcb.agr.ehime-u.ac.jp,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GluGlnGluIleThrValAlaGluGlyIleGluTyrGlnAspAlaIleValGluThrAla
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                                                                                                                                                                                                                                                                                      ValCysValAspPheThrTyrGlnTyrThrLeuLeuValAspGlyPheGlyLeuAspPro
      GlyLysLysTyrAspLeuTyrValHisSerTyrLeuArgTyrGlyAsnAspAlaAlaArg
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                                                                      263 VallysilePhelysThrThrAspGlyAlaAlaSerProCysLeuLeuAlaGlyTyrGlu
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Acta Physiol. Plant. 20, 3-13 (2001)
2 (bases 1 to 1651)
Shibata,K. and Abe,S.
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AVVEDAGSTGER HYVHFNONLDLAHGKGVERYNK TPGLESSYANNEDDAKKSLIFL
LAGEDVVPODLOPKTPVKLGATGLRILNGDASEKILGSYRDMLSNRSTFNVOPDAV
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VCMDLIYQYVLLVDGFGLDPLQKITSGKEIEYQDAIVEBARSTYPFLDKKNVASY
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/product="S-type apyras"
/protein_id="BAB40230.1"
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                       488 TTCAACGTTCAACGAGGGAGTTCTATAATTGATGGAACCCAAGAAGGTTCTTATCTA
                                                                                                                        ValileAspLeuGlyGlyAlaSerValGlnMetAlaTyrAlaValSerArgAsnThrAla
                                                                                                                                                  608 GTAATAGATCTTGGAGGTGGATCAGTTCAAATGGCGTATGCAGTATCAAAGAAAACTGCT
                                                                                                                                                                                                                                                                                                                      GCAGAGATTITGAAGCICACTCCTCGTICTCCTAACCCTIGCCTTTAGCTGGATTITAGT
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                                                                TrpValThrValAsnTyrLeuLeuGlyLysLeuGlyLysLysPheThrLysThrValGly
                                                                                            548 regereacacraracearregeaarreaceaaaagracacacaaaaacacracaa
                                                                                                                                                                                   LysAsnAlaProLysProProGlnGlyGluAspProTyrMetLysLysLeuValLeuLys
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| ABTGCATGGATCTTATATATATGTGTTACTCGTTGATGGATTTGGTCTTGATCCA
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|28 AAGATTTTCCTAAAACAAGAGAAATTTCCTCTTACGCTGTCGTATTCGATGCTGGTAGC
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GTTTACCCT-----ACACAAATGGAGTTCCTTATTAAACTTATCACTTTTCTACTATTTT
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Fax:+81-89-946-9853)
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Matches:
Conservative:
Mismatches:
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/mol_type="mRNA"
/strain="Alaska"
/db_xref="taxon:3888"
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TTTAATAAATGCAAAAACACAATTCGTAAGGCTCTTAAGGTTGAACTATCCATGTCCATAT
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GluLysAlaAlaGluSerLeuIleProLeuLeuGluGluAlaGluAspValValProGlu
                                                             GluLeuHisProLysThrProLeuLysLeuGlyAlaThrAlaGlyLeuArgLeuAsp
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ADGDDPYIKKVVLKGIPYDLYVHSYLHFGRBASRABILKLTPRSPNCTLLAGFNGIYT
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VCMDLIYQYVLLVDGFGLDPLQKITSGKEIEYQDAIVBAAWPLGNAVBAS
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Submitted (10-SEP-2001) Tomonori Shiraishi, Okayama Univers
1-1-1 Tsushima naka, Okayama city, Okayama 700-8530, Japan
(B-mail:tomoshirecc.okayama-u.ac.jp, Tel:81-86-251-8311,
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                                                                                                                                                                                                                       Fax:81-86-251-8311)
Location/Qualifiers
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Shiraishi,T.
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Aaf63422 Human CD3
Aaf63386 Human CD3
Aad31693 Human CD3
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 NBP46 (root lectin) cDNA.
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Database :

Score

Result

WPI; 1999-167136/14. P-PSDB; AAW85684.

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The NBP46 root lectin is instrumental in recognising and binding to nitrogen fixing rhizobial bacteria via a lectin-carbohydrate interaction. The production of transgenic plants comprising an expression cassette expressing the NBP46 root lectin is advantageous since it would mean that non-leguminous plants could fix nitrogen from the atmosphere, lessening the need for the addition of nitrogen containing fertilizer to soil. This would lead to higher crop yields where soil has been overplanted and replenishment of the depleted soil with usable nitrogen. Alternatively, replension of NBP46 can be used to modulate oligosaccharide signalling in the plant. The nucleic acid sequences can be used to inhibit expression of an endogenous gene and also to suppress endogenous NBP46 gene
New polynucleotides encoding Nod factor binding lectins - useful for production of transgenic plants which are able to fix nitrogen.
                                                                                                                                                                                                        Claim 3; Page 42; 57pp; English.
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Sequence 1643 BP; 505 A; 317 C; 347 G; 474 T; 0 U; 0 Other;

equence to to be been as	ment Scores: 2.03e-235 Length: 1643 No.: 2404.00 Matchs: 462 int Similarity: 100.00% Conservative: 0 Local Similarity: 100.00% Mismatches: 0 Match: 2 Gaps: 0	7-631-2 (1-462) x AAX08522 (1-1643)	1 MetAsnIrpValTrpProLysThrLysSerMetSerPheLeuLeuLeuLeulleThrPheLeu	51 ATGAATTGGGTGTGGCCAAAGACAAAGAGCATGAGCTTCCTACTCCTCATCATTTCTA		111 CTCTTCTCATTGCCAAAACTTTCTTCTTCGCAATATGTTGGAACAGTALCTACTAAAA	41 HisArglysIleLeuProAsnGlnGluLeuLeuThrSerTyrAlaValIlePheAspAla (171 CATCGTAAGATACTTCCCAACCAGGAACTCCTTACCTCTTACGCTCTCATCTTTGATGCT	61 GlySerSerGlySerArgValHisValPheAspRlheAspGlnAsnLeuAspLeuLeuHis {	231 GGTAGCTCTGGGAGTCGTGTCCATGTCTTCAATTTTGACCAGAACTTAGATCTCCTGCAC	81 IleGlyAsnAspLeuGluPheThrLysLysIlelysProGlyLeuSerSerTyrAlaAsp	291 ATTGGCAATGACCTCGAGTTTACAAAAAGATCAAACCCGGTTTGAGCTCATACGCTCAT	101 LysprogluLysAlaAlaGluSerLeuIleProLeuLeuGluGluAlaGluAspValVal	351 AAGCCTGAAAAAGCTGCAGAATCTCTCATTCCACTTTTGGAGGAAGCTGAAGATGTTGTC	121 ProGluGluLeuHisProLysThrProLeuLysLeuGlyAlaThrAlaGlyLeuArgLeu	411 CTTGAGGAACTGCACCCCAAGACACCCCTTAAGCTTGGGGCAACAGCAGGTTTGAGGCTC	141 LeuAspGlyAspAlaAlaGluLysIleLeuGlnAlaValArgGluMetPheArgAsnArg	471 ITGGATGGGGATGCTGTGTAAAGATATTGCAAGCGGTTAGGGAAATGTTCAGGAACAGA	161 SerSerLeuSerValGlnProAspAlaValSerVallleAspGlyThrGlnGluGlySer	531 AGTICCCIGAGGGIICAACCIGAIGCAGTAICTGTTAITGAIGGAACCCAAGAAGGIICT	181 TyrLeuTrpValThrValAsnTyrLeuLeuGlyLysleuGlyLyslysPheThrLysThr	591 TACTTATIGGGTTACAGTTAACTATCTGTTAGGAAAGTTGGGAAAGAAGATTACAAAAACT	
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                                                          /note= "Lectin/nucleotide phosphohydrolase"
50. .194
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195. .1436
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   iocation/Qualifiers
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                                             'product= "LNP"
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P-PSDB; AAU78818.
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                                                                                                                                                                                                                                                                                                  The NBP46 root lectin is instrumental in recognising and binding to nitrogen fixing rhizobial bacteria via a lectin-carbohydrate interaction. The production of transgenic plants comprising an expression cassette expressing the NBP46 root lectin is advantageous since it would mean that non-leguminous plants could fix nitrogen from the atmosphere, lessening would lead to higher crop yields where soil has been overplanted and replentishment of the depleted soil with usable nitrogen. Alternatively, expression of NBP46 can be used to modulate oligosaccharide signalling in the plant. The nucleic acid sequences can be used to inhibit expression of an endogenous gene and also to suppress endogenous NBP46 gene
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                                                                                                                                                                                                                                       New polynucleotides encoding Nod factor binding lectins - useful for production of transgenic plants which are able to fix nitrogen.
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                               NBP46; lectin; Rhizobium; leguminous plant; transgenic plant; nitrogen; nitrogen; sertilizer; ss.
                  ProLeuGlyThrAlaileGluAlaIleSerSerLeuProLysPheAsnArgLeuMetTyr
                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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1152. .1559
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1023. .1151
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266 PheLysThrThrAspGyAlaAlaSerProcySLoubeuAddity figure 202	4	4	, 4514 TGACCAAAGTTACTTTTCCTCACTGAGTTCTATTGAAATGCAGAAACTTGTTGCAGATA 4573	4574 TITIAAAIACAIAITAAGIGITITIGICAGIACIGCAITIGITITITAGIGALTITCAAGICG 463 282	4634 AGTITITICITGAAGCAITAAAGCIGCAAATAACAIGIGGGICTTITITICIALCIITAAA 4693 283 ASDILETVIAGTYXSexGlyGluSerTyrAsnileTyrGlyProThiSexGlyAlaAsn 302 4604 GANATATACAGATATHCCGAAGAACGIACAATATATATATATAGACCACTICIGGIGCCAAC 4753	303	323	343 ValValThrSerAlaPheTyrTyrArgSerSerGlu35 	354	4994 TGCTAATTTTGTTGTTTTTTAGGTTTGTTGTCACCTCCTCCCCAATTCCAAAAAAAA	388 ThrPheProAsnValGluLysAspLysLeuProPheValCysValAspPheThrTyrGln 407 388 [408 TYThrleuleuvalaspGlyPhe	415	Db 5294 TTGGCadGCCTAGATCCAGAGCAAGATTACAGTGGCAGAAGGAATTGAATATCAAGAT 5353 Qy 434 AlaIleValGluThrAlaTrpProLeuGlyThrAlaIleGluAlaIleSerSerLeuPro 453
QY ATCATTCATATAGGAAGGAACAATTATCATTTCTAAAATATATTTATAATCTC 3313 QY	m	51 433	1 E	DD TITAATTATTATTATTATAAAATAAATTTTATTTTTAAATTTT	Db TTTTTAATTTTAATAAAAATATAATATTATTAATAATTATTATTATTTAATTTT	TTTATTAATAATAATAATAAATAAATAATATATATTTTATGTTATTA	TITAATTATACATATGTATTTTTTGCAAATTTTTACCTTTTAAGCGGAGAAGATGA 3733 OY	AGGGCATAAATTGTTCTCGAAATTAGTTATATTTTGTTCAATTTTAACAAAATCATCTCA 3793 Oy		CAATTIGAAAGACGAAAGCTAAACCAAATTTAGAAAAAGTAAAAACTIGGTTAACT 3973 QY	TTATAACGAATGTCAGAAAAAAAGGTAGGTATGTTATAAATACTTCTGATATCAAAATGG 4033 QY	409	ATGAATGCTTACTTTTTAAGATATTTATAGATATCTATAATCCATTGAAGTTCAGTGT 4153 QY	273 65

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The invention describes a method of modulating mycorrhizal infection by introducing into a plant an expression cassette comprising a plant promoter operably linked to a heterologous LNP (lectin/nucleotide phosphotydrolase) polymucleotide, or its complement. The LNP's described in the invention are involved in binding a variety of carbohydrates, catalysing the dephosphorylation of nucleotide di- and tri-phosphates and are suspected to be involved in oligosaccharide signalling, important for the interaction of mycorrhizal fungi and plants. The method is useful to increase mycorrhizal infection (by increasing expression of the polynucleotide), resulting in increased uptake of nutrients by plants and better growth/development, but antisense (or other methods of)
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/note= "No start or stop codon given"
/transl except= (pos:22. .24, aa:Xaa)
/transl except= (pos:1411. .1413, aa:Xaa)
/transl except= (pos:1453. .1455, aa:Xaa)
/note= "Xaa= Stop codon"
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Location/Qualifiers
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                                                                                                                                                                                            DNA; 1489
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P-PSDB; AAU78820.
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AC ABK1
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DB DNA
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Sequence 1489 BP; 437 A; 284 C; 324 G; 444 T; 0 U; 0 Other;

modulate mycorrhizal infection in plants

1489

Length:

6.68e-162

Alignment Scores: Pred. No.:

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33 GIGTICALGITAALGCCIGCIAICTCTTCCTCCCAAIATCTCGGAAACAACATTCTCAIG 132
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                                                                                                            -----ACTAAAGCCATGGACTTCTTAATTAGTCTCATGACCTTT
                                                                                                                                                                                                          313 GCTGCTAATCCTGAAGAAGCTGCAGAATCTCTGATTCCACTTCTAAAAGAAGCAGAAAAT
                                                                                           1 MetAsnTrpValTrpProLysThrLysSerWetSerPheLeuLeu---LeulleThrPhe
                                                                                                                                             20 LeuLeuPheSerLeuProLysLeuSerSerSerGinTyrValGlyAsnSerIleLeuLeu
                                                                                                                                                                                                                                                                                                            40 AsnHisArgLysIleLeuPro---AsnGlnGluLeuLeuThrSerTyrAlaValIlePhe
                                                                                                                                                                                                                                             59 AspAlaGlySerSerGlySerArgValHisValPheAsnPheAspGlnAsnLeuAspLeu
                                                                                                                                                                                                                                                                                           79 LeuHisIleGlyAsnAspLeuGluPheThrLysLysIleLysProGlyLeuSerSerTyr
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 319
68
71
8
            Conservative:
Mismatches:
 Matches:
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                                                                    US-09-657-631-2 (1-462) x ABK11100 (1-1489)
1684.00
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Best Local Similarity:
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/note= "These bases represent nucleotides missing from
the sequence given in the specification. They are
included to maintain the nucleotide numbering given in
the specification for this sequence"
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/note= "These bases represent nucleotides missing from
                                                                                                                                           ValThrProProAsnSerLysAsnArgProLeuAspPheGluThrAlaAlaLysGlnAla
                                                                                                                                                                                         CysSerLeuThrPheGluGluAlaLysSerThrPheProAsnVal---GluLysAspLys
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 LeuProPheValCysValAspPheThrTyrGlnTyrThrLeuLeuValAspGlyPheGly
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                                                     GlnLysAsnLeuvalValThrSerAlaPheTyrTyrArgSerSerGluValGly-
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The NBP46 root lectin is instrumental in recognising and binding to nitrogen fixing rhizobial bacteria via a lectin-carbohydrate interaction. The production of transgenic plants comprising an expression cassette non-leguminous plants could fix nitrogen from the atmosphere, lessening the need for the addition of nitrogen containing fertilizer to soil. This would lead to higher crop yields where soil has been overplanted and replenishment of the depleted soil with usable nitrogen. Alternatively, expression of NBP46 can be used to medulate oligosaccharide signalling in the plant. The nucleic acid sequences can be used to inhibit expression of an endogenous gene and also to suppress endogenous NBP46 gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MetAsnTrpValTrpProLysThrLysSerMetSerPheLeuLeu---LeuIleThrPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ValValProGluGluLeuHisProLysThrProLeuLysLeuGlyAlaThrAlaGlyLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AsnHisArglys1leLeuPro---AsnGlnGluLeuLeuThrSerTyrAlaValllePhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59 AspAlaGlySerSerGlySerArgValHisValPheAsnPheAspGlnAsnLeuAspLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GATGCTGGTAGCACTGGAAGCAGAGTCCATGTCTACAATTTTGATCAGAACTTAGATCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    313 GCTGCTAATCCTGAAGAAGCTGCAGAATCTCTGATTCCACTTCTAAAAGAAGCAGAAAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----ACTAAAGCCATGGACTTCTTAATTAGTCTCATGACCTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             79 LeuHisIleGlyAsnAspLeuGluPheThrLysLysIleLysProGlyLeuSerTyr
                                                                                                                                                                                                          New polynucleotides encoding Nod factor binding lectins - useful for production of transgenic plants which are able to fix nitrogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0 U; 10 Other;
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318
67
73
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Matches:
Conservative:
Mismatches:
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1674.00
82.62%
68.24%
69.63%
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97US-00907226
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GlySerTyrLeuTrpValThrValAsnTyrLeuLeuGlyLysLeuGlyLysPheThr
                                        LysThrValGlyValIleAspLeuGlyGlyAlaSerValGlnMetAlaTyrAlaValSer
                                                                     219 ArgAsnThrAlaLysAsnAlaProLysProProGlnGlyGluAspProTyrMetLysLys
                                                                                                       AGGAACACAGCTAAAAATGCTCCAAAANNNCCTGAAGGAGAGAGATCCATACATAAAGAAG
                                                                                                                          LeuValLeuLysGlyLysLysTyrAspLeuTyrValHisSerTyrLeuArgTyrGlyAsn
                                                                                                                                  GAAGCATTTCGTGCANNNATTTTCAAGGTCGCTGGTGGTTCTGCTAATCCTTGCATTTTA
                                                                                                                                                       AspalaalaargValLysIlePheLysThrThrAspGlyalaAlaSerProCysLeuLeu
                                                                                                                                                                                                 |||||||:::::
|GCTGGCTTTGAYGGGCATATACATATTCCGGAGCAGAGTATAAGGTCTCGGCCCCAGCT
                                                                                                                                                                                                                                                                                                                                               CysSerLeuThrPheGluGluAlaLysSerThrPheProAsnVal---GluLysAspLys
                                                                                                                                                                                                                                                                                                                                                         |||
|TGTAAAACAAATCTTGAGGATGCAAAATGCAAATACCCAGATCTTTATGAGAAGACAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                          GluThrAlaTrpProLeuGlyThrAla11eGluAla11eSerSerLeuProLysPheAsn
                                                                                                                                                                                                                              ProCysSerHisGluAsnCysThrPheGlyGlyIleTrpAspGlyGlybysGlySerGly
                                                                                                                                                                                                                                                             GlnLysAsnLeuValValThrSerAlaPheTyrTyrArgSerSerGluValGly---Phe
                                                                                                                                                                                                                                                                                                                 ValThrProProAsnSerLysAsnArgProLeuAspPheGluThrAlaAlaLysGlnAla
                                                                                                                                                                                                                                                                                                                                                                                                                    LeuAspProGluGlnGluIleThrValAlaGluGlyIleGluTyrGlnAspAlaIleVal
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ВР

CDNA; 1458

AAX08528 standard;

entry) cDNA.

(first

19-JUL-1999

AAX08528

AAX08528 1D AAX0 XX AC AAX0 XX DT 19-J XX DE NBP4

NBP46 (root lectin)

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The NBP46 root lectin is instrumental in recognising and binding to nitrogen fixing rhizobial bacteria via a lectin-carbohydrate interaction. The production of transgenic plants comprising an expression cassette expressing the NBP46 root lectin is advantageous since it would mean that non-leguminous plants could fix nitrogen from the atmosphere, lessening the need for the addition of nitrogen containing fertilizer to soil. This would lead to higher crop yields where soil has been overplanted and replenishment of the depleted soil with usable nitrogen. Alternatively, the plant. The nucleic acid sequences can be used to inhibit expression of an endogenous gene and also to suppress endogenous NBP46 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               123
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NBP46; lectin; Rhizobium; leguminous plant; transgenic plant; nitrogen; nitrogen; nitrogen; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27 LeuSerSerSerGlnTyrValGlyAsnSerIleLeuLeuAsnHisArgLysIleLeuPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AsnGlnGluLeuLeuThrSerTyrAlaValIlePheAspAlaGlySerArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ValHisValPheAsnPheAspGlnAsnLeuAspLeuLeuHisIleGlyAsnAspLeuGlu
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                   /product= "NBP46 root lectin"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps:
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                                                                                                                             complement (1. .1380)
                                                                                                          Location/Qualifiers
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                                                                                                                                                                                                                                                                                                 98WO-US016261
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1654.50
82.75%
67.03%
68.82%
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                                                                                                                                                                                                                                                                                                                                                                                                                               Murphy JB;
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Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P-PSDB; AAW85685
                                                                sativa.
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Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1458
                                                                                                                                                                                                                                                                                            05-AUG-1998;
                                                                                                                                                                                                                                                                                                                                      06-AUG-1997;
                                                                                                                                                                                                           WO9907223-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alignment Scores:
                                                                                                                                                                                                                                                       18-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                          Etzler ME,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          87
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Sequence 1458 BP; 438 A; 267 C; 309 G; 444 T; 0 U; 0
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transl_except= (pos:1024.
/transl_except= (pos:1378.
/transl_except= (pos:1408.
/transl_except= (pos:1435.
/note= "Xaa= Stop codon"
                                                                                                                                                                                                                                                                                                                                                                                                      Modulating mycorhizal infection, useful
                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 3; Page 32-34; 37pp; English.
                                                                                                                                                    corniculatus var. japonicus.
                                  BP.
                                                                                                                                                                                                                                                                                                                              06-SEP-2000; 2000US-00657631,
                                                                                                                                                                                                                                                                                                              06-SEP-2001; 2001WO-US028165
                                   DNA; 1458
                                                                   (revised)
(first entry)
                                                                                                                                                                                                             partial
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                                                                                                                                                                                                                                                                                                                                                               Roberts NJ;
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                                   standard;
                                                                                                                                                                                                                                                                                                                                                                                                              transforming plan
phosphohydrolase.
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                                                                                                                                                                                                                                                                               WO200220725-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alignment Scores:
                                                                   29-AUG-2003
18-JUN-2002
                                                                                                                                                                                                                                                                                               14-MAR-2002
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                                    ABK11099
                                                     ABK11099;
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                            ABK11099
                    RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AlaLysSerThrPheProAsnValGluLysAspLysLeuProPheValCysValAspPhe
                                                                       GluLysileLeuGlnAlaValArgGluMetPheArgAsnArgSerSerLeuSerValGln
                                                                                                           GAAAAGATATTGCAAGCGACAAGGAATATGTTCAGCAACAGAAGTACCCTCAACGTTCAA
                                                                                                                                       AsnTyrLeuLeuGlyLysLeuGlyLysLysPheThrLysThrValGlyValIleAspLeu
                                                                                                                                                                       GGAGGTGGTTCAAATGACATATGCAGTGTCAAAGAAAAAAGCAGAAAAATGCTCCT
                                                                                                                                                                                                                                        TTGTTGACAAGATCAAACCAGGTTTGAGTGCATATGGGGATAATCCTGAACAAGCAGGA
                             GluserLeuIleProLeuLeuGluGluAlaGluAspValValProGluGluLeuHisPro
                                        LysThrProLeuLysLeuGlyAlaThrAlaGlyLeuArgLeuLeuAspGlyAspAlaAla
                                                                                                                                                                                                                                LysProProGlnGlyGluAspProTyrMetLysLysLeuValLeuLysGlyLysLysTyr
                                                                                                                             ProAspAlaValSerValIleAspGlyThrGlnGluGlySerTyrLeuTrpValThrVal
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The invention describes a method of modulating mycorrhizal infection by introducing into a plant an expression cassette comprising a plant promoter operably linked to a heterologous LNP (lecth/nucleotide phosphotydrolase) polynucleotide, or its complement. The LNP's described in the invention are involved in binding a variety of carbohydrates, catalysing the dephosphorylation of nucleotide di- and tri-phosphates and are suspected to be involved in oligosaccharide signalling, important for the interaction of mycorrhizal fungi and plants. The method is useful to increase mycorrhizal infection (by increasing expression of the polynucleotide), resulting in increased uptake of mutrients by plants and better growth/development, but antisense (or other methods of) suppression of LNP expression is also contemplated. This sequence encodes the Lotus japonicus lettin/nucleotide phosphohydrloase (LNP) that can be used to modulate mycorrhizal infection in plants. (Updated on 29-AUG-2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 β
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DNA encoding Lotus japonicus lectin/nucleotide phosphohydrolase,
                                                                     Lectin/nucleotide phosphobyrdolase; LNP; mycorrhizal infection; carbohydrate binding protein; nucleotide dephosphorylation; oligosaccharide signalling; nutrient uptake; plant growth;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          *tag= a
product= "LNP"
/note= "Lectin/nucleotide phosphohydrolase"
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= (pos:1024. 1026, aa:Ala)

= (pos:1378 . 1380, aa:Xaa)

= (pos:1448. 1410, aa:Xaa)

= (pos:1435. 1437, aa:Xaa)
                                                                                                                                                                                                                          plant development; antisense technology; gene;
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347 AlapheTyrTyrArgSerSerGluvalGlyPheValThrPro-----ProAsnSerLys 364
                                                                                                         AsnArgProLeuAspPheGluThrAlaAlaLysGlnAlaCysSerLeuThrPheGluGlu 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 drug resistance in target bacteria, yeast, plant or mammalian cells by altering the ATP gradient across the biological membrane of the target cell. The method is useful for modulating drug resistance of cells. It is useful for increasing the sensitivity of cells to chemotheraputic and antibiotic agents and increasing resistance to herbicides. The present antibiotic agents and increasing resistance to herbicides. The present cellular phosphatase). This sequence was used in the present invention to modulate drug resistance. Note: The present sequence is not shown in the specification, but is referred to via its GenBank accession number
                                                                         385 AlaLysSerThrPheProAsnValGluLysAspLysLeuProPheValCysValAspPhe
         PheglyglylleTrpAspGlyGlyLysGlySerGlyGlnLysAsnLeuValValThrSer
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                                                                                                                                                                                                          405 ThrTyrGlnTyrThrLeuLeuValAspGlyPheGlyLeuAspProGluGlnGluIleThr
                                                                                                                                                                                                                                                                          The present invention relates to a method for increasing or decreasing
                                                                                                                                                                                                                                                                                                                         Increasing or decreasing drug resistance in target bacteria, yeast, or mammalian cells comprises altering ATP gradient across biological membrane of target cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gradient; chemotheraputic;
                                                                                                                                                                                                                                                                                                           445 AlalleGluAlaileSerSerLeuProLysPheAsnArgLeuMetTyrPheIle
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antibiotic; herbicide; extra-cellular phosphatase; ds.
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                                                                                                                                                                                                                                                                ValHisValPheAsnPheAspGlnAsnLeuAspLeuLeuHisIleGlyAsnAspLeuGlu
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TTGAGGATGCGAATCTACTTATCCATTTCTTGATAAGAAAATGTAGCTTCATATGTA 1223
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                                                                                           GlnGlu1]eThrValAlaGluGlyIleGluTyrGlnAspAlaIleValGluThrAlaTrp
304 AsnGluCysArgAspLeuAlaLeuGlnIleLeuArgLeuAsnGluProCysSerHisGlu
                        344 ValThrSerAlaPheTyrTyrArgSerSerGluValGlyPheVal-----ThrProPro
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                                                                    AsnCysThrPheGlyGlyIleTrpAspGlyGlyLysGlySerGlyGlnLysAsnLeuVal
                                                                                                                                                                                                                                                                                    PheglugluhlalysSerThrPheproAsnValGlulysAspLysLeu---ProPheVal
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The present invention provides the protein and coding sequences of a pea protein with nucleotide triphosphate decomposing activity. The gene can be used for conferring blight resistance on a plant. The present sequence is one version of the coding sequence of the invention
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                                                           PheAsnGluCysArgAspLeuAlaLeuGlnIleLeuArgLeuAsnGluProCysSerHis 322
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AspileTyrArgTyrSerGlyGluSerTyrAsnIleTyrGlyProThrSerGlyAlaAsn
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/product= "blight resistance protein"
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ThrPheGluGluAlaLysSerThrPheProAsnValGluLysAspLysLeu---ProPhe 399
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                  GCCGAGATTTTGAAGCTCACTCCTCGTTCTCCTAACCCTTTGCCTTTAAGCTGGATTTAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              142
                                            The present invention provides the protein and coding sequences of a pea protein with nucleotide triphosphate decomposing activity. The gene can be used for conferring blight resistance on a plant. The present sequence is one version of the coding sequence of the invention
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                                                                                                                                                                                                                                                                              LysileLeuProAsnGlnGluLeuLeuThrSerTyrAlaValilePheAspAlaGlySer
                                                                                                                                                                                                                                                                                                                                                    SerGlySerArgValHisValPheAsnPheAspGlnAsnLeuAspLeuLeuHisIleGly
                                                                                                                                                                                                                          VallrpProLysThrLysSerMetSerPheLeuLeu---LeuIleThrPheLeuLeuPhe
                                                                                                535 A; 308 C; 306 G; 548 T; 0 U; 0 Other;
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Matches:
Conservative:
Mismatches:
Indels:
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                           4; Page 12-13; 20pp; Japanese
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990 GluSerTyrAsnIleTyrGlyProThrSerGlyAlaAsnPheAsnGluCysArgAspLeu 309
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                  AspGlyAlaAlaSerProCysLeuLeuAlaGlyTyrGluAspIleTyrArgTyrSerGly
                                                              ValHisSerTyrLeuArgTyrGlyAsnAspAlaAlaArgValLysIlePheLysThrThr
                                                                                                                   838 AGAAGATTTAAGGCAACTGCTTACACTTCTGGTGCAAACTTTAATAAATGCAAAAAAACACA
                                                                                                                                      310 AlaLeuGlnIleLeuArgLeuAsnGluProCysSerHisGluAsnCysThrPheGlyGly
                                                                                                                                                                                   330 ileTrpAspGlyGlyLysGlySerGlyGlnLysAsnLeuValValThrSerAlaPheTyr
                                                                                                                                                                                                                              350 TyrArgSerSerGluValGlyPheVal-----ThrProProAsnSerLysAsnArgPro
                                                                                                                                                                                                                                                                           368 LeuAspPheGluThrAlaAlaLysGlnAlaCysSerLeuThrPheGluGluAlaLysSer
                                                                                                                                                                                                                                                                                                                                       ThrPheProAsnValGluLysAspLysLeu---ProPheValCysValAspPheThrTyr
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                                                                                    The present invention provides the protein and coding sequences of a pea protein with nucleotide triphosphate decomposing activity. The gene can be used for conferring blight resistance on a plant. The present sequence is one version of the coding sequence of the invention
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                                                                                                                                                                                                                                                                                                                                                                                      GARATTECTCTTACGCTGTAGTATTCGATGCCGGTAGCACTGGTAGTCGCATTCATGTT 177
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TIGCAATCGGIAAGGGATAIGCTGAGCAGAGGAGTACCTICAACGTICAACCAGACGCA
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                              New blight-resistant polypeptide useful for giving blight resistance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TCAGTTCAAATGGCGTATGCAGTATCAAAGAAAACTGCTAAAAATGCTCCAAAAGTTGCA
                                                                                                                                              Sequence 1368 BP; 422 A; 260 C; 275 G; 411 T; 0 U; 0 Other;
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Mismatches:
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                                                                                                                                                             The NBP46 root lectin is instrumental in recognising and binding to nitrogen fixing rhizobial bacteria via a lectin-carbohydrate interaction. The production of transgenic plants comprising an expression casette expressing the NBP46 root lectin is advantageous since it would mean that non-leguminous plants could fix nitrogen from the atmosphere, lessening the need for the addition of nitrogen containing fertilizer to soil. This would lead to higher crop yields where soil has been overplanted and replenishment of the depleted soil with usable nitrogen. Alternatively, expression of NBP46 can be used to modulate oligosaccharide signalling in the plant. The nucleic acid sequences can be used to inhibit expression of an endogenous gene and also to suppress endogenous NBP46 gene expression. This DBX sequence also isolated from D. biflorus is also involved in oligosaccharide signalling
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production of transgenic plants which are able to fix nitrogen.
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                                                                           TATTCAAAGACGGTTGCTGTAGTTGACCTAGGTGGATCTGTTCAAATGGCTTACGCA
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                                                   GlnGluGlySerTyrLeuTrpValThrValAsnTyrLeuLeuGlyLysLeuGlyLysLys
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to identifying a stress condition to which a plant cell has been exposed, comprising: (a) contacting nucleic acid representative of expressed polymuclocides in the plant cell with an array or probes representative of the plant cell genome; and (b) detecting a profile of expressed polymucleotides in the plant cell plantacteristic of a stress response. The method is useful in the plant cell production of transgenic plants, cells and seeds and in producing plants with increased tolerance to abiotic stress. The present sequence is that of a Arabidopsis thalians stress regulated gene (ABZ12196-ABZ17574) used in methods of the invention. Note: The sequence data for this patent is not represented in the printed specification but is based on sequence information supplied to Derwent by the European Patent Office
                                                                                                                                                                                                                                                                                                                                                                                                           Identifying a stress condition to which a plant cell has been exposed and producing plants with increased tolerance to these abiotic stresses.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 144; SEQ ID NO 1888; 577pp + Sequence Listing; English.
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                 ds.
           thaliana; plant; gene; stress; transgenic;
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(SYGN ) SYNGENTA PARTICIPATIONS AG.
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26-JAN-2001; 2001US-0264647P.
22-JUN-2001; 2001US-0300111P.
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                                               Arabidopsis thaliana
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The invention relates to a novel isolated polynucleic acid segment modulated within a cell by posttranscriptional gene silencing (PTGS). The invention specifically relates to a method to identify an expression product that is modulated by PTGS. The polynuclectide is useful for modulating the gene expression within a cell by PTGS, by introducing the polynucleic acid into a cell and expressing the nucleic acid segment in the cell to form a product. The polynucleic acid segment is also useful for augmenting a cell genome, and for augmenting a plant genome, by contacting a plant cell with the segment to produce a transformed plant cell, and growing the transformed plant cell to produce a differentiated transformed plant. The segments session in ABZ421017 - ABZ42142 represent segments of A. thaliana cDNA modulated by PTGS
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                                                                                                          Posttranscriptional gene silencing; PTGS; plant; transformation; gene;
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94 GlyLeuSerSerTyrAlaAspLysProGluLysAlaAlaGluSerLeuIleProLeuLeu
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                               GlnAsnLeuAspLeuLeuHisIleGlyAsnAspLeuGluPheThrLysLysIleLysPro
                                            GluGluAlaGluAspValValProGluGluLeuHisProLysThrProLeuLysLeuGly
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GlyAsnSerIleLeuLeuAsnHisArgLysIleLeuProAsnGlnGluLeuLeuThrSer 53

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GlyLeuSerSerTyrAlaAspLysProGluLysAlaAlaGluSerLeuIleProLeuLeu

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391 GACAAAGCATCTGTTCCCCGTCAGCTGCGTCCAAAGACACATGTCAGAGTTGGG

AlaThrAlaGlyLeuArgLeuLeuAspGlyAspAlaAlaGluLysIleLeuGlnAlaVal

114 GluGluAlaGluAspValValProGluGluLeuHisProLysThrProLeuLysLeuGly

ArgGluMetPheArgAsnArgSerSerLeuSerValGlnProAspAlaValSerVallle

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AspGlyThrGlnGluGlySerTyrLeuTrpValThrValAsnTyrLeuLeuGlyLysLeu

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CTCATTGATGGATTCGGATTGGAGCCATCACAGACAATAACGTTAGTGAAGAAGGTCAAA 1350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to a method (M1) for identifying genes involved in plant resistance or response to pathogenic infection. M1 comprises identifying a gene whose expression is significantly altered in the incompatible interaction of plant gene expression relative to expression of the gene in an uninfected plant, in a mutant plant that does not express a gene associated with response to pathogenic infection, or in a corresponding incompatible compatible interaction. (M1) is useful for conferring resistance to resistance or tolerance to a plant to element in the interaction or in the present sequence was used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      t 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Identifying at least one gene involved in plant resistance or response pathogenic infection for conferring resistance or tolerance to a plant bacterial, fungal or viral infection by determining or detecting plant
                       TyrGlnAspAlaileValGluThrAlaTrpProLeuGlyThrAlaileGluAlaileSer
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Whitham S, Xie Z,
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LeuLeuLeulleThrPheLeuLeuPheSerLeuProLysLeuSerSerGerGlnTyrVal
 Length:
Matches:
Conservative:
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                                                                                US-09-657-631-2 (1-462) x ADA68447 (1-1419)
8.46e-121
1281.50
74.15%
54.88%
53.31%
                                  Best Local Similarity:
Query Match:
                     Percent Similarity:
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Alignment Scores:

150 33

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - nucleic search, using frame_plus_p2n model

August 19, 2004, 14:05:21; Search time 3567.58 Seconds (without alignments) 3867.136 Million cell updates/sec

Run on:

US-09-657-631-2
2404
1 MNWVWPKTKSMSFLLLITFL.....GTAIEAISSLPKFNRLMYFI 462 Title: Perfect score:

0.5 Xgapop 10.0 , Xgapext Ygapop 10.0 , Ygapext Fgapop 6.0 , Fgapext Delop 6.0 , Delext **BLOSUM62** Scoring table: Sequence:

27513289 segs, 14931090276 residues Searched:

55026578 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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EST:* Database :

em_esthum:
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em_estru:
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em_estro: em_estba:*

gb_est3:* gb_est4:* 10:

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em gss mus:* em_gss_pro:*

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gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

HQ165194 743 bp mRNA linear EST 25-APF EST611063 KVKC Medicago truncatula cDNA clone pKVKC-6G5, mRNA Sequence. BQ165194 LOCUS DEFINITION

RESULT 1

ACCESSION

EST 25-APR-2002

BQ165194 BQ165194.1 GI:20307369

VERSION KEYWORDS SOURCE ORGANISM

Medicago truncatula (barrel medic)
Medicago truncatula
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;

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clone_lib="KV3"
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Unpublished (2001)
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/note="Vector: pBluescript SK-; Site 1: BcoRI; Site 2:
XhoI; cDNA was prepared from polyA+ enriched RNA. The cDNA
was directionally ligated into the Unizap XR vector from
Stratagene and packaged using Gigapack III Gold packaging
Stratagene and packaged using Gigapack III Gold packaging
extracts. Plasmids containing cDNA inserts were excised
from the recombinant lambda-Zap phage using Ex-assist
helper phage and propagated in XLOLR cells."
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                                    Town, C.D., Van Aken, S.
                                                                                                                  1 (bases 1 to 743)
VandenBosch, K., Endre, G., Silverstein, K., Town, C.D., Van Ake Utterback, T., Cheung, F. and Fraser, C.M.
The Medicago truncatula 'kiloclone' set; ESTs selected and re-arrayed from various libraries
Unpublished (2002)
Contact: VandenBosch K.
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Matches:
Conservative:
Mismatches:
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/mol type="mRNA"
/cultivar="A17"
                                                                                                                                                                                                                                                                                                                                                           'tissue_type="mixed tissues"
                                                                                                                                                                                                                                                                                                                                                                         /dev stage="various stages"
/lab_host="XLOLR"
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COMMENT
                                       AUTHORS
                           REFERENCE
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/note="Vector: pBluescript SK -; Site_1: EcoRI; Site_2: XhoI; cDNA was prepared from polyA+ enriched RNA. The cDNA was directionally lagated into the Unizap KR vector from Stratagene and packaged using Gigapack III Gold packaging extracts. Plasmids containing cDNA inserts were excised
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M24 5' end,
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
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                                                                                                                                                                                                                                                                                540 GGGAAATTGGGAAAAAATTCACAAAAACAGTGGGAGTAATGGATCTTGGAGGTGGATCA
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151 GlnAlaValArgGluMetPheArgAsnArgSerSerLeuSerValGlnProAspAlaVal
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VandenBosch, K., Endre, G., Hur, J., Beremand, P., Town, C.D.,
Bowman, C.L., Craven, M.B., Cho, J. and Fraser, C.M.
ESTS from roots of Medicago truncatula 72 h after Rhizobium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Department of Plant Biology
University of Minnesota
22 BioSci Center, 1445 Gortner Ave, St. Paul, MN 55108,
Tel: 612 624 2755
Pax: 612 625 1738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: kvandenb@cbs.umn.edu
M392896e TIGR sequence name: MTEBP84TK More information
available at: www.medicago.org
Seq primer: Skmod (CTA gAA CTA gtg gAT CC).
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BG644489 1inear EST
ESTS06108 KV3 Medicago truncatula cDNA clone pKV3-37M24
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/organism="Medicago truncatula"
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Utterback, T., Cho, J.
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/dev stage="Roots harvested at 10, 17, 22, 31 and 38 days
post-inoculation with Glomus versiforme. The library was
made from a mixture of RNA from each of these stages."
/lab_host="E. coli strain XLOLR"
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                                                                                                                    1 (bases 1 to 760)
Harrison,M.J., Liu,J., Town,C.D., Van Aken,S., Utterback,T., Chand Fraser,C.M.
and Fran roots of Medicago truncatula after colonization with Glomus versiforme, 2001
Unpublished (2001)
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                                                                                                                                                                                                                                                                              Contact: Harrison M.J.
Plant Biology Division
The Samuel Roberts Noble Foundation
The Samuel Roberts Noble Foundation
Tel: 580-221-5810
Fax: 580-221-7380
Email: miharrison@noble.org
Noble EST name: N379883e TIGR sequence name: MTDBQ16TK More information is available at: http://www.medicago.org
Seq primer: SKmod (CTA gAA CTA gtg gAT CC).
Location/Qualifiers

    .760
/organism="Medicago truncatula/Glomus versiforme

                               Medicago truncatula/Glomus versiforme mixed EST library Medicago truncatula/Glomus versiforme mixed EST library Eukaryota; mixed EST libraries.

1 (bases 1 to 760)
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/cultivar="Medicago_truncatula_genotype_A17"
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/clone="pMHAM-15D7"
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BG584413.1 GI:13599477
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S Korth, K., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J., Flores, H.R., Inman, J.T., Weller, J.W. and May, G.D.
Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula insect herbivory library

L Unpublished (2000)
Contact: Korth K
Dept. of Plant Pathology
University of Arkansasia
217 Plant Science Building, Fayetteville, AR 72701, USA
Tel: 501 575 500
Email: kkorth@comp.uark.edu
Insert Length: 651 Srd Error: 0.00
Email: kkorth@comp.uark.edu
Insert Length: 651 Srd Brror: 105
Plate: 105 row: B column: 12
Seq primer: TCACAGGAAAAGCTATGAC.
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NF105B12IN1F1101 Insect herbivory Medicago truncatula cDNA clone
NF105B12IN 5', mRNA sequence.
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
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                                                                                                                                                                                              LeuArgLeuLeuAspGlyAspAlaAlaGluLySIleLeuGlnAlaValArgGluMetPhe
                                                                                       158 ArgAsnArgSerSerLeuSerValGlnProAspAlaValSerValIleAspGlyThrGln
                                                                                                                                           GluGlySerTyrLeuTrpValThrValAsnTyrLeuLeuGlyLysLeuGlyLysLysPhe
                                                                                                                                                                                                                              ThriysThrValGlyValIleAspLeuGly-GlyAlaSerValGlnMetAlaTyrAlaVa
                                                                                                                                                                                                                                                     ACAAAAACAGTGGGAGTAATGGATCTTGGAGGGTGGATCAGTTCAAATGGCATATGCAGT
                                                                                                                                                                                                                                                                                                                                 sLysLeuValLeuLysGlyLysLysTyrAspLeuTyrValHisSerTyrLeuArgTyrGl
TATGCAAATGATCCGGAACAAGCTGCAAAATCTTTGATTCCACTTCTACAACAAGCAGAA
                                                                                                                                                                                                                                                                               1SerArgAsnThrAlaLysAsnAlaProLysProProGlnGlyGluAspProTyrMetLy
                       AspvalvalProGluGluLeuHisProLysThrProLeuLysLeuGlyAlaThrAlaGly
                                      tissue type="local and systemic /dev stage="mature" /clone_lib="Insect herbivory"
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'db_xref="taxon:3880"
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BI267324.1 GI:14872249
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mRNA linear EST 24-APR-2002
Medicago truncatula cDNA clone
/note="Vector: Lambda Zap; Library was produced from fully expanded M. truncatula leaves of plants fed upon by spodoptera exigna (beet armyworm) for 24 hours. Systemic (undamaged leaves from injured plants) and wounded leaves were harvested and pooled."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     200
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Medicago truncatula
Bukaryota, Viridiplantae, Streptophyta, Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rTyrLeuTrpValThrValAsnTyrLeuLeuGlyLysLeuGlyLysLysPheThrLysTh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            200 rvalGlyvalIleAspLeuGlyGlyAlaServalGlnMetAlaTyrAlaValSerArgAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TACAGCTAAAAATGCTCCAAAAGTTGCTGATGGAGAAGATCCATACATTAAGAAGCTTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     425 TTATCTCTGGGTGACAGTTAACTATGCGGAAATTGGGAAAAATTCACAAAAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              <u> AGTGGGAGTAATGGATCTTGGAGGTGGATCAATTGGCATATGCAGTGTAAGTA</u>
                                                                                                                                                                                                                                                                                                                                                                                                      120 lproglugluLeuHisProLysThrProLeuLysLeuGlyAlaThrAlaGlyLeuArgLe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   220 nThrAlaLysAsnAlaProLysProProGlnGlyGluAspProTyrMetLysLysLeuVa
                                                                                                                                                                                                                                                                                                                                                                                                                                                         sIledlyAsnAspLeuGluPheThrLysLysIleLysProGlyLeuSerSerTyrAlaAs
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                                                                                                                                                                                                                                                                                                            HisArgLysIleLeuProAsnGlnGluLeuLeuThrSerTyrAlaValIlePheAspAla
                                                                                                                                                                                                                                                                                                                               GlyserSer-GlyserArgValHisValPheAsnPheAspGlnAsnLeuAspLeuLeuHi
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165
28
21
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                                                                                                                                                Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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NF068A12FLIF1097 Developing flower.
NF068A12FL 5', mRNA sequence.
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/dev_stage="mature"
/clone_lib="Insect herbivory"
/clone_lib="Insect herbivory"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EST 18-JUL-2001
    GluLeuHisProLysThrProLeuLysLeuGlyAlaThrAlaGlyLeuArgLeuLeuAsp 142
                                                                                          143 GlyAspAlaAlaGluLysIleLeuGlnAlaValArgGluMetPheArgAsnArgSerSer 162
                                                                                                                                                                        163 LeuSerValGlnProAspAlaValSerValIleAspGlyThrGlnGluGlySerTyrLeu 182
                                                                                                                                                                                                                                                                                                                    202
                                                                                                                                                                                                                                                                                                                                                          613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Medicago truncatula (barrel medic)
Medicago truncatula
Bukaryota, Viridiplantaes, Streptophyta, Embryophyta, Tracheophyta,
Spernatophyta, Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
Medicago.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            656 bp mRNA linear BST 18-JUL-20
NF093BH0IN1F1089 Insect herbivory Medicago truncatula cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Korth, K., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J., Flores, H.R., Inman, J.T., Weller, J.W. and May, G.D.
Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula insect herbivory library
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                     494 TICAAIGITCAACCIGAIGCAGITICTAITAITGAIGGAACCCAAGAAGGITCITAATCIC
                                                                                                                                                                                                                                                                                                         183 TrpValThrValAsnTyrLeuLeuGlyLysLeuGlyLysLysPheThrLysThrValGly
                                                                                                                                                                                                                                                                                                                                                                                            203 VallleAspLeuGlyGlyAlaSerValGlnMetAlaTyrAlaValSerArgAsnThrAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Korth K.
Dept. of Plant Pathology
University of Arkansas
217 Plant Science Building, Fayetteville, AR 72701, 171: 501 575 5191
Fax: 501 575 7601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="local and systemic leaves"
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157
34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: kkorth@comp.uark.edu
Insert Length: 656 Std Error: 0.00
Plate: 093 row: B column: 10
Seg primer: TCACACAGGAAACAGCTATGAC.
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/db_xref="taxon:3880"
/clone="NF093B101N"
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824.50
88.43%
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                                                                 123
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/clone_lib="Developing flower."
/clone_lib="Developing flower."
/note="Vector: Lambda Zap; cDNA was prepared from polyA+enriched, pooled samples of equivalent amounts of total RNA from very young, developing, fully-opened flowers and flowers transitioning into pods. The cDNA was directionally ligated into the Uni-Zap XR vector (Stratagene) and packaged using the Gigapack III Gold packaging extracts. Phagemids containing cDNA inserts were in vivo excised from the recombinant Uni-Zap XR vector using ExAssist helper phage and the E. coli strain XLI-Blue MRF. (Stratagene). Excised plasmids were plated
                                                           Bell, C.J.,
eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LysIleLeuProAsnGlnGluLeuLeuThrSerTyrAlaValIlePheAspAlaGlySer 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SerGlySerArgValHisValPheAsnPheAspGlnAsnLeuAspLeuHisIleGly 82
                                                    Torres-Jerez, I., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C., Stores, H.R., Imman, J.T., Weller, J.W. and May, G.D.
Styressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula flower library
Unpublished (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 ValTrpProLysThrLysSer---MetSerPheLeuLeuLeuIeThrPheLeuLeuPhe
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159
35
1
1
                                                                                                                                                                                                                         73402,
                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="NF068A12FL"
/tissue_type="Developing flowers"
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Matches:
Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                      organism="Medicago truncatula"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches:
                                                                                                                                                                                                                                                                              Email: gdmay@noble.org
Insert Length: 673 Std Error: 0.00
Plate: 068 row: A column: 12
Seg primer: TCACACAGGAAACAGCTATGAC.
                                                                                                                                                                           Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OX
Tel: 580 221 7381
Fax: 580 221 7380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels:
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/db_xref="taxon:3880"
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833.50
88.18%
72.27%
34.67%
                                 (bases 1 to 673)
                                                                                                                                                                                                                                                                                                                                                                               1, .673
                                                                                                                                                            Contact: May GD
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                     source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No.:
                                                      AUTHORS
                                                                                                                                  JOURNAL
                                      REFERENCE
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                                                                                               TITLE
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USA

73402,

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Location/Qualifiers
1. 660
/ organism="Medicago truncatula"
/mol_type="mRNA"
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/db_xref="caxon:380"
/clone="NPOSFF11ST"
/tissue_type="stem"
The Samuel Roberts Noble Foundation 2510 Sam Noble Parkway, Ardmore, OK 7340: Tel: 580 221 7302
Fax: 580 221 7380
Email: radixon@noble.org
Medicago Genome Initiative accession: MG
Insert Length: 660 Std Brror: 0.00
Plate: 055 row: F column: 11
Seq primer: TCAGACAGGABACAGCTATGAC.
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Contact: Dixon RA
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GATCAGCGCTCCAAGACACCCCATTAGACTTGGGGCAACAGCAGCAGTTTAAGGCTTTTGAAT
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Plant Biology Division
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824.50
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658 bp mRNA linear EST 18-JUL-2001
clone NF038F11FL 5', mRNA sequence.
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                                                                                                            427 GCATCCGCTCCACCTTCCGGTGCTAGTTACTCAAAATGCAAGGATGATGCAGTGAAAGCC 486
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
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Flores,H.R., Inman,J.T., Weller,J.W., May,G.D. and Harrison,M.J.
Expressed Sequence Tags from the Samuel Roberts Noble Foundation
Medicago truncatula phosphate-starved leaf library
Unpublished (2000)
                                                                                                                                                       314 LeuArgLeuAsnGluProCysSerHisGluAsnCysThrPheGlyGlyIleTrpAspGly
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/note="Vector: Lambda Zap; At the trifoliate stage,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Harrison MJ
Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USJ
Tel: 580 221 7325
Fax: 580 221 7380
Email: mjharrison@noble.org
Insert Length: 658 Std Error: 0.00
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Seq primer: TCACACAGGAAACAGCTATGAC.
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Zea mays cDNA, mRNA sequence
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Xhoi"
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Dr. Joachim Messing's lab
Waksman Institute, Rutgers University
190 Frelinghuysen Rd., Piscataway, NJ 08854, USI
Tel: 732-445-3801
Fax: 732-445-5735
Email: jlai@waksman.rutgers.edu
Seq primer: T3.
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EL01N0520B01.b Endosperm_5 Ze
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Korth, K., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J., Flores, H.R., Inmai, J.T., Weller, J.W. and May, G.D.

Flores, H.R., Inmai, J.T., Weller, J.W. and May, G.D.

Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula insect herbivory library

Unpublished (2000)

Contact: Korth K

Dept. of Plant Pathology
University of Arkansas

217 Plant Science Building, Fayetteville, AR 72701, USA

Tel: 501 575 5191

Fax: 501 575 7601

Email: Kkorthogoomp. wark.edu
                                                                                                                                                                                                                                                                                                                                           /mol_type="mrna"]
/db xref="taxon:3880"
/clone="NP065A041N"
/tissue type="local and systemic leaves"
/dev stage="mature"
/clone lib="Insect herbivory"
/clone lib="Insect herbivory"
/note="vector: Lambda Zap; Library was produced from fully expanded M. truncatula leaves of plants fed upon by expanded M. truncatula leaves of plants fed upon by expanded I eaves from injured plants) and wounded leaves were harvested and pooled."
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eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
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      truncatula plants were transplanted to phosphate-free sand and grown for a further 30 days. During this 30 day period, the plants were fertilized twice weekly with 1/2 Hoadjands solution containing only 20uM potassium phosphate. RNA was prepared from above ground tissues."
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
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NF067E07INIF1054 Insect herbivory Medicago truncatula cDNA clone NF067E07IN 5', mRNA sequence.
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Korth, K., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J.,
Flores, H.R., Inman, J.T., Weller, J.W. and May, G.D.
Expressed Sequence Tags from the Samuel Roberts Noble Foundation
Medicago truncatula insect herbivory library
Unpublished (2000)
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217 Plant Science Building, Fayetteville, AR 72701, Tel: 501 575 5191
Eax: 501 575 7601
Email: kkorth@comp.uark.edu
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/dev stage="mature"
/clone_lib="Insect herbivory"
/note="vector: Lambda Zap; Library was produced from fully expanded M. truncatula leaves of plants fed upon by Spodoptera exigua (beet armyworm) for 24 hours. Systemic fundamaged leaves from injured plants) and wounded leaves were harvested and pooled."
                                                                                                                                                                                                                                                                                                     NP003H05IN1F1048 Insect herbivory Medicago truncatula cDNA clone NP003H05IN 5', mRNA sequence.
182
                                                                                                   551
                                                                                                                                      202
                                                                                                                                                             Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids I, Fabales, Fabaceae, Papilionoideae, Trifolieae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Korth, K., Soct, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J., Flores, H.R., Inman, J.T., Weller, J.W. and May, G.D.
Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula insect herbivory library
Unpublished (2000)
Contact: Korth K
Dept. of Plant Pathology
University of Arkansas
217 Plant Science Building, Fayetteville, AR 72701, USA
Tel: 501 575 5191
                                                                            TrpValThrValAsnTyrLeuLeuGlyLysLeuGlyLysLysPheThrLysThrValGly
                                                       163 LeuSerValGlnProAspAlaValSerValIleAspGlyThrGlnGluGlySerTyrLeu
                                                                                                                                                                                                   203 ValileAspLeuGly-GlyAlaSerValGlnMetAlaTyrAlaVal 217
                                                                                                                                                                                                                          651
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Matches:
Conservative:
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Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                              Medicago truncatula (barrel medic)
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/db_xref="taxon:3880"
/clone="NF003H05IN"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: kkorth@comp.uark.edu
Insert Length: 651 Std Er
                                                                                                                                                                                                                                                                                                                                                                                          BG449019.1 GI:13367800
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801.50
88.15%
72.04%
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                                                                                                                                183
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JOURNAL COMMENT

TITLE

FEATURES

REFERENCE AUTHORS

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

LOCUS DEFINITION

RESULT 11

g à

 $\overset{\sim}{\circ}$ g à a BG449019

FEATURES

ValTrpProLysThrLysSer---MetSerPheLeuLeuLeulleThrPheLeuLeuPhe 22

Query Match:

Pred. No.:

Score:

ORIGIN

438 162

Tracheophyta;

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/dev_stage="mature"
/done_lib="Insect herbivory"
/note="Vector: Lambda Zap; Library was produced from fully expanded M. truncatula leaves of plants fed upon by Spodoptera exigua (beet armyworm) for 24 hours. Systemic (undamaged leaves from injured plants) and wounded leaves were harvested and pooled."
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rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
                                                                                                                                                                      Korth, K., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J., Flores, H.R., Inman, J.T., Weller, J.W. and May, G.D. Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula insect herbivory library Unpublished (2000)
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                                                                                              Embryophyta;
                                                                                                                                                                                                                                                                                              University of Arkansas
17 Plant Science Building, Fayetteville, AR 72701,
721: 501 575 7601
Fax: 501 575 7601
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                              Medicago truncatula
Eukaryota, Viridiplantae; Streptophyta;
                                                                                                                                                                                                                                                                                                                                                            Email: kkorth@comp.uark.edu
Insert Length: 665 Std Error: 0.00
Plate: 098 row: A column: 09
Seg primer: TCACACAGGAAACAGCTATGAC.
                                                            Medicago truncatula (barrel medic
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1. .665
NF098A09IN 5', mRNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="NF098A09IN"
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Dept. of Plant Pathology
                             GI:14871547
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800.50
86.92%
71.03%
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EST.
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DB:
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AUTHORS
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NF098A09INIF1069 Insect herbivory Medicago truncatula cDNA clone
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Conservative:
Mismatches:
Indels:
                    /organism="Medicago truncatula"
/mol_type="mRNA"
/db_xref="taxon:3880"
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33.05%
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1 (bases 1 to 625)
        Best Local Similarity:
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BI272922.1
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                                                                                                                                                                                                                                                                                                                                                              B1265005 664 bp mRNA linear BST 18-JUL-2001
NF004G10IN1F1084 Insect herbivory Medicago truncatula cDNA clone
142
                                                              143 GlyAspAlaAlaGluLysIleLeuGlnAlaValArgGluMetPheArgAsnArgSerSer 162
                                                                                                                   163 LeuSerValGinProAspAlaValSerValIleAspGlyThrGlnGluGlySerTyrLeu 182
                                                                                                                                                                                              560
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Korth, K., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J., Flores, H.R., Inman, J.T., Weller, J.W. and May, G.D. Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula insect herbivory library Unpublished (2000)
Contact: Korth K
Dept. of Plant Pathology
                                           GluLeuHisProLysThrProLeuLysLeuGlyAlaThrAlaGlyLeuArgLeuLeuAsp
                                                                                                                                                                                                                   TrpValThrValAsnTyrLeuLeuGlyLysLeuGlyLysLysLysPheThrLysThrValGly
                                                                                                                                                                                                                                              SOI TICAATGTTCAAGGGGGTTTCTATTATGATGGAACCCAAGAAGGTTCTTATCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        University of Arkansas 1
217 Plant Science Building, Fayetteville, AR 72701, USA
Tel: S01 575 5191
Fax: S01 575 7601
                                                                                                                                                                                                                                                                          203 ValileAspLeuGlyGlyAlaSerValGlnMetAlaTyrAla 216
                                                                                                                                                                                                                                                                                                    621 GTAATGGATCTTGGANGTGGATCANNTCAAATGGNNTATGCA 662
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Conservative:
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Plate: 004 row: G column: 10
Seg primer: TCACACAGGAAACAGCTATGAC.
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Medicago truncatula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                         NF004G10IN 5', mRNA sequence
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BI265005.1 GI:14867791
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Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula flower library
Unpublished (2001)
Contact: May GD
Plant Biology Division
The Samuel Roberts Noble Foundation
                                                                                                                                                                                                                                                                                                                 71 AATATACTCACCAAT---CGTAAAATATTTCCAAAACAAGAAACTCTAACCTCGTACGCT 127
                                                                                                                                                                                                                                                                                                                                                                                                                                     187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SerSerTyrAlaAspLysProGluLysAlaAlaGluSerLeuIleProLeuLeuGluGlu 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    248 AGTGCATACGCAGATAATCCAAAGGAAGCAGCAGAGTCTCTGATTCCACTTTTAGAGCAA 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            116 AlagluAspValValProGluGluLeuHisProLysThrProLeuLysLeuGlyAlaThr 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             136 AlaglyLeuArgLeuLeuAspGlyAspAlaAlaGluLysIleLeuGlnAlaValArgGlu 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    176 ThrGlnGluGlySerTyrLeuTrpValThrValAsnTyrLeuLeuGlyLysLeuGlyLys 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       196 LysPheThrLysThrValGlyVallleAspLeuGlyGlyAlaSerValGlnMetAlaTyr 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Medicago truncatula
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids I, Fabales, Fabaceae, Papilionoideae, Trifolieae,
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                                                                                                                                                                                                                                                                                                                                                                        ValllePheAspAlaGlySerSerGlySerArgValHisValPheAsnPheAspGlnAsn 75
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NF091F05FL 5', mRNA sequence.
                                                                                                                                                                                         11 CTCATCACATTTCTACTCTTCTTGATGCCTACAATCTTCCTCCCCCAATATCTTGGAAAC
                                                                                                                                                           LeulleThrPheLeuLeuPheSerLeuProLysLeuSerSerGlnTyrValGlyAsn
                                                                                                                                                                                                                                                                 SerileLeuLeuksnHisArgLysIleLeuProAsnGlnGluLeuLeuThrSerTyrAla
                                                                                                                                                                                                                                                                                                                                                                                                                  128 GICGICITIGAIGCIGGIAGCACCGGIAGCCGIGIICACTGICACCAITITIGAICAGAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LeuAspLeuLeuHisIleGlyAsnAspLeuGluPheThrLysLysIleLysProGlyLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     216 AlaValSerArgAsnThrAlaLysAsnAlaProLysProProGlnGlyGluAspPro 234
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Mismatches:
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/dev.stage="Developing flowers and flowers
/dev.stage="Developing fully-opened flowers and flowers
in early transition into pods."
/clone lib="Developing flower"
/clone lib="Develo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ArgieuleuAspGlyAspAlaAlaGluLysIleLeuGlnAlaValArgGluMetPheArg 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GlySerTyrLeuTrpValThrValAsnTyrLeuLeuGlyLysLeuGlyLysLysPheThr 198
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Fax: 580 221 7380
Email: gdmay@noble.org
Insert Length: 65 Std Error: 0.00
Plate: 091 row: F column: 05
Seg primer: TCACACAGAGAACAGCTATGAC.
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Matches:
Conservative:
Mismatches:
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/mol_type="mRNA"
/db_xref="taxon:3880"
/clone="NF091F05FL"
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Gaps:
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278
                                                    279 AlaglyTyrGluAspIleTyrArgTyrSerGlyGluSerTyrAsnIleTyrGlyProThr 298
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                                                                   259 AspalaalaargValLysIlePheLysThrThrAspGlyAlaAlaSerProCysLeuLeu
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Sequence Sequence

Minimum DB Maximum DB

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Seguence

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Sequence

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APPLICANT: Etzler, Marilynn E.
APPLICANT: Murphy, Judith B.
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: A No. 6465716 Factor Binding Protein From Legume Roots
FILE REFERENCE: 023070-07981003
CURRENT APPLICATION NUMBER: US/09/129,112
CURRENT FILE OF THE CALIFY APPLICATION NUMBER: US/09/129,112
                                                                                                                                                                                                                                                                                                                                       Sequence
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WHER INFORMATION: NB946 (DB46) No. 6465716 factor binding lectin NAMB/KEY: mat peptide LOCATION: (195)..(1436)
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Mismatches:
Indels:
Gaps:
US-09-557-800C-52
US-09-37C-625A-26
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US-09-608-285A-4
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US-09-370-625A-4
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PRIOR FILING DATE: 1997-08-06
NUMBER OF SEQ ID NOS: 19
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
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Patent No. 6465716
GENERAL INFORMATION:
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Listing first 45 summaries
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APPLICANT: Etzler, Marilynn E.
APPLICANT: The Regents of the University of California
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: A No. 6465716 Factor Binding Protein From Legume Roots
FILE REFERENCE: 023070-079810US
CURRENT APPLICATION NUMBER: US/09/129,112
CURRENT FILING DATE: 1998-08-04
PRIOR FILING DATE: 1997-08-06
NUMBER OF SEQ ID NOS: 19
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 3
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                                                                   CysvalAspPheThrTyrGlnTyrThrLeuLeuValAspGlyPheGlyLeuAspProGlu
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  ProAsnSerLysAsnArgProLeuAspPheGluThrAlaAlaLysGlnAlaCysSerLeu
                       1131 CCCAATTCCAAAAATCGCCCTCTGGATTTTGAAACTGCAGCTAAACAACTTGTAGTTTA
                                                  ThrpheGluGluAlaLysSerThrPheProAsnValGluLysAspLysLeuProPheVal
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OTHER INFORMATION: genomic sequence of NBP46
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US-09-1129-112-3
Sequence 3, Application US/09129112
Patent No. 6465716
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ORGANISM: Dolichos biflorus
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LOCATION: (945)...(1022)
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LOCATION: (1023)..(1151)
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NAME/KEY: exon
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                                               trictrgacaacaacaaccaccrrrcacrararccacararccrcaraccaacca
                                                                          GluserLeulleProbeuLeuGluGluAlaGluAspValValProGluGluLeuHisPro
                                                                                       LysThrProLeuLysLeuGlyAlaThrAlaGlyLeuArgLeuLeuAspGlyAspAlaAla
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184 GTCCATGTTTACCATTTTGATCAGAACTTAGATCTACTTCACATTGGCAATGATATTGAG
                       PheThrLysLysIleLysProGlyLeuSerSerTyrAlaAspLysProGluLysAlaAla
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                  LeuProPheValCysValAspPheThrTyrGlnTyrThrLeuLeuValAspGlyPheGlY
                                                                                                                                                                                                                                                                                 APPLICANT: Etzler, Marilynn E.
APPLICANT: Etzler, Marilynn E.
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: A No. 6465716 Factor Binding Protein From Legume F
FILE REFERENCE: 023070-07981005
CURRENT APPLICATION NUMBER: US/09/129,112
CURRENT FILING DATE: 1998-08-04
PRIOR FILING DATE: 1997-08-06
NUMBER OF SEQ ID NOS: 19
SOFTWARE: Patentin Ver. 2.1
                                                                     LeuAspProGluGluGluIleThrValAlaGluGlyIleGluTyrGl
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Mismatches:
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                                                                                                                                                                                       NAME/KEY: CDS

LOCATION: (1)...(1458)

OTHER INFORMATION: full length cl.

NAME/KEY: CDS

LOCATION: (13)...(1380)

CTHER INFORMATION: NBF46

NAME/KEY: modified base

LOCATION: (1)...(1458)

COTHER INFORMATION: n = g, a, c or US-09-129-112-8
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Query Match:
DB:
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Pred. No.:
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117 GluAspValValProGluGluLeuHisProLysThrProLeuLysLeuGlyAlaThrAla 136
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                                                                                                                                                                                                     Length:
Matches:
LOCATION: (1133)..(1151)

MAMB/KAY: priner. bind
LOCATION: (1227)..(1247)

OTHER INFORMATION: DBX12 primer
NAME/KAY: priner bind
NAME/KAY: priner bind
LOCATION: (1414)..(1434)

LOCATION: (1414)..(1434)

OTHER INFORMATION: DBXbottom primer
US-09-129-112-18
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                                                                                                               Generace 18, Application US/09129112
GENERAL INCORATION:
GENERAL INFORMATION:
APPLICANT: Etzler, Marilynn E.
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: AN O. 6465716 Factor Binding Protein From Legume Roots
FILE REFERENCE: 023070-079810US
CURRENT FILING DATE: 1998-08-04
PRIOR PILING DATE: 1998-08-04
PRIOR PILING DATE: 1997-08-06
NUMBER OF SEQ ID NOS: 19
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 18
              LOCATION: (1)..(1404)
OTHER INFORMATION: DBX gene involved in oligosaccharide signaling
NAMB/KEY: sig_peptide
LOCATION: (1)..(60)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: DBX7-for/rev primer NAME/KEX: primer bind LOCATION: (667). (685) OTHER INFORMATION: DBX1-for/rev primer NAME/KEX: primer bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: [688]. (704)
OTHER INFORMATION: DBX2-for/rev primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: Complement((1075)..(1093))
OTHER INFORMATION: DEX11 primer
NAME/KEY: primer_bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCATION: Complement (766)..(785))
OTHER INFORMATION: DBX10 primer
NAME/KEY: misc. feature
LCCATION: (856)..(857)
OTHER INFORMATION: splice site
NAME/KEY: primer bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: Complement((1)...(zz),
OTHER INFORMATION: DEXtop primer
NAME/KEY: primer bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: (1071)..(1072)
OTHER INFORMATION: splice site
NAME/KEY: primer_bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: (274)...(291)
OTHER INFORMATION: DBX8 primer
NAME/KEY: primer bind
LOCATION: (297)...(314)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: primer bind
LOCATION: (878)...(896)
OTHER INFORMATION: DBX5 primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: (955). (972)
OTHER INFORMATION: DBX4 primer
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OTHER INFORMATION: DBX6 primer
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                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Dolichos biflorus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: (61)..(1404)
NAME/KEY: primer_bind
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: mat peptide LOCATION: (61)..(1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (952)
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---HisArgLys

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657 236 717 777

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GluaspileTyrargTyrSerGlyGluSerTyrasnileTyrGlyProThrSerGlyAla 301
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136
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Matches:
Conservative:
Mismatches:
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Gaps:
                   09/118,205
PRIOR FILING DATE: 1998-07-24
PRIOR APPLICATION NUMBER: 09/116
PRIOR FILING DATE: 1998-07-16
NUMBER OF SEQ ID NOS: 60
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 48
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506.00
49.40%
32.61%
21.05%
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                                                                                                                                                         US-09-608-285A-48
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Pred. No.:
                                                                                                       LENGTH: 2693
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                                                                                                                       TYPE: DNA
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                                                                                                                                                                                                                            AATGCAACATGCTCTTATAAGGATTGCACTTTCGGAGGCATATGGAATGCCGGTGGTGGA 1017
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                                                       LeuleuAlaGlyTyrGluAspIleTyrArgTyrSerGlyGluSerTyrAsnIleTyrGly 296
                                                                                                                                                                                            AsnGluProCysSerHisGluAsnCysThrPheGlyGlyIleTrpAspGlyGlyIvsGly 336
                                                                                                                                                   837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             435 IleValGluThrAlaTrpProLeuGlyThrAlaIleGluAlaIleSerSerLeuProLys
     ProThrSerGlyAlaAsnPheAsnGluCysArgAspLeuAlaLeuGlnIleLeuArgLeu
                                                                                                                                                                                                                                                                SerGlyGlnLysAsnLeuValValThrSerAlaPheTyrTyrArgSerSerGluValGly
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APPLICANT: Wenge, Julio
APPLICANT: Yeung, George
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CD39-LIKE
TITLE OF INVENTION: POLYPEPTIDES
TITLE OF INVENTION: POLYPEPTIDES
TITLE OF INVENTION: POLYPEPTIDES
FILE REPERBNCE: 28110/36570
CURRENT APPLICATION NUMBER: US/09/608,285A
CURRENT APPLICATION NUMBER: 09/583,231
PRIOR FILING DATE: 2000-06-30
PRIOR PAPLICATION NUMBER: 09/557,800
PRIOR APPLICATION NUMBER: 09/557,800
PRIOR PILING DATE: 2000-01-11
PRIOR PILING DATE: 2000-01-11
PRIOR PILING DATE: 1099-07-06
PRIOR PILING DATE: 1999-07-16
PRIOR PILING DATE: 1999-07-16
PRIOR PILING DATE: 1999-07-16
PRIOR APPLICATION NUMBER: 09/273,447
PRIOR APPLICATION NUMBER: 09/273,447
PRIOR PILING DATE: 1999-07-09
PRIOR PILING DATE: 1999-07-09
PRIOR PILING DATE: 1999-07-09
PRIOR PILING DATE: 1999-07-09
PRIOR PILING DATE: 1999-07-09
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PRIOR PILING DATE: 1999-02-04
PRIOR PILING DATE: 1999-02-04
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TTTGAGAATTAATGTATTTCCTT 1401
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patent No. 6335013
GENERAL INFORMATION:
APPLICANT: Ford, Jo
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US-09-608-285A-48
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Best Local Similarity: 32.61% Mismatches: 151 Query Match: 21.05% Indels: 60 DB: 4 Gaps: 13	-09-657-631-	Oy 54 TyralavalilePheAspAlaGlySerSerGlySerArgValHisValPheAsnPheAsp 73 Db :::::::::::::::::::::::::::::::::::	74GlnAsnLeuAspLeuLeuHisIleGlyAsnAspLeuGluPheThrLys	Db 442 CGGCCCCCCAGAGAAACTCCCACGTTAACCACGAAACCTTCAAA 486 Ov 90 invsileivsProclvienSerSerTvralaaeniwebrachuiwealaalaason.com	487 GCAGTGAAGCCAGGTCTTTCTGCCTATGATGATGTTGAAAAGGGGCTCAGGAATC	110	09		667 CTGCAGAAGGTGAAAGTATTTAAAGCATCGCCTTTCCTTGTAGGGGATGACTGT 72	DD 724 GTTTCCAFCAFGAAAGAGAAAGAGGTTTGGGGGGGGGAACAACATGATTCGG 183		Db 784 ACAGGCAGCTTGAAAACTCCAGGAGGAGCAGCGTGGGCATGCTGGACTTGGGCCAAGGA 843	Oy 210 SerValGlnMetAlaTyrAlaValSerArgAsnThrAlaLysAsnAlaProLysProPro 229	230	Db 901GGCTACCTGACGGCACTGCGGGATGTTTAACAGGACCTACAAGTCTAT 948	OY 250 ValHisSerTyrLeuArgTyrGlyAsnAspAlaAlaArgValLysIlePheLysThrThr 269	949	OY 270 AspOlyAlaAlaSerProCysLeuLeuAlaGlyTyr 281 :::	301	CAGAAAGCAGCGGCA 1	Qy 302 AsnPheAsnGluCysArgAspLeuAlaLeuGlnIleLeuArgLeu 316	Db 1129 AGCCTGCACGAGCTGCCGCAGAGTGTCAGAGGTCCTTCAAAACAGAGTGCACAGG 1188	Qy 317 AsnGluProCysSerHisGluAsnCysThrPheGlyGlyIleTrpAspGlyGlyLysGly 336	Db 1189 ACGGAGGAAGTGAAGCAT1206	Oy 337 SerGlyGlnLysAsnLeuValValThrSerAlaPheTyrTyrArgSerSerGluValGly 356	Db 1207GIGGACITCTAIGCITICTCCTACIATHACGACCITGCAGCIGGIGGGC 1257	Qy 357 PheValThrProProAsnSerLysAsnArgProLeuAspPheGluThrAlaAlaLys 375 ::: }	
Qy 302 AsnPheAsnGluCysArgAspLeuAlaLeuGlnIleLeuArgLeu 316 :::	Gly	337 SerGlyGl	1207GIGGACITCTATGCTTTCTCCTACTATTACGACCTTGCAGCTGGTGGGGC	Sy firevalinition to the state of the state	376 GlnAlaCysSerLeuThrPheGluGluAlaLysSerThrPheProAsnValGluLysAsp	1318 TACGTGTGTCGGACCCTGGAGACACACGCGCAGAGCAGC	VY 356 LYSLeukrophewill of Cysvalaspherintryrdintyrihrleuleuwalaspdlyphe 415 Db 1357CCCTTCTCATGCATGGACCTCACCTACGTCAGCTGTACTCCAGGAGTTC 1407	GlyLeuAspProGluGluGluIleThrValAlaGluGlyIleGluTyzGlnAspAlaIle	Db 1456 GTTGGGGCTGGGCTGGGCTGGGCCTGTGGTTTTTTCATALLESETSETLEU 452	RESULT 7	. Section 1970 -	; GENERAL INFORMATION: ; APPLICANT: Ford, John	; APPLICANT: Mulero, Julio ; APPLICANT: Yeung, George ; TITLE OF INVENTION: Methods and Materials Relating to CD39-Like	; TITLE OF INVENTION: Polypeptides ; FILE REFERENCE: 28110/36457 : CHRRENT ADDITCATON MINURED: 114/00/557	CURRENT FILING DATE: 2000-04-25; PRIOR APPLICATION NUMBER: 09/481,238	; PRIOR FILING DATE: 2000-01-11 ; PRIOR APPLICATION NUMBER: 09/370,265			; FRICK AFFLICATION NUMBER: 09/2/3447; PRIOR FILING DATE: 1999-03-19; PRIOR PADPLICATION NUMBER: 06/1-0440			ING DATE: 1998-0. SEQ ID NOS: 56	; SOFTWARE: Patentin Ver. 2.0 ; SEQ ID NO 48 . : Favour: 2.0	; TYPE: DIA	; ORGANISM: Homo sapiens US-09-557-800C-48	Scores:	Fred. NO.: 6.16e-52 Length: 2693 Score: 506.00 Matches: 136 Percent Similarity: 49.40% Conservative: 70	

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1198 AGCCTGCACGAGCTGTGTGCTGCCAGAGTGTCAGAGGTCCTTCAAAACAGAGTGCACAGG 1257
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SerValGlnMetAlaTyrAlaValSerArgAsnThrAlaLysAsnAlaProLysProPro 229
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                                                                                                                                                                                                                                                                                                                                                                              LeuGlnAlaValArgGluMetPheArgAsnArgSerSerLeuSerValGlnProAspAla 169
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                                                                                                                          LysllelysproglyLeuSerSerTyrAlaAspLysProgluLysAlaAlaGluSerLeu 109
                                                                                                                                                                                                              IleProLeuLeuGluGluAlaGluAspValValProGluGluLeuHisProLysThrPro 129
                                                                                                                                                                                                                                                                                             LeuLysLeuGlyalaThrAlaGlyLeuArgLeuLeuAspGlyAspAlaAlaGluLysIle 149
                                                                                                                                                                                                                                                                                                                       282 GluAspileTyrArgTyrSerGlyGluSerTyrAsnIleTyrGlyProThrSerGlyAla
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151 TACGGGATCATGTTGATGCAGGAAGCACTGGCACCCGAGTACACGTCTTCCAGTTCACC
                                                                                                                                                       GCAGTGAAGCCAGGTCTTTCTGCCTATGCTGATGTTGAAAAGAGCGCTCAGGAATC
                                                                                                                                                                                                                                          -GlnAsnLeuAspLeuLeuHisIleGlyAsnAspLeuGluPheThrLys
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                              376 GlnAlaCysSerLeuThrPheGluGluAlaLysSerThrPheProAsnValGluLysAsp
                                                                                                                  LysLeuProPheValCysValAspPheThrTyrGlnTyrThrLeuLeuValAspGlyPhe
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TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CD39-LIKE
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CD39-LIKE
TITLE OF INVENTION: POLYPEPTIDES
FILE REFERENCE: 23110/3670
CURRENT APPLICATION NUMBER: US/05/631
PRIOR PELLING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 09/557,800
PRIOR APPLICATION NUMBER: 09/557,800
PRIOR PLILING DATE: 2000-04-25
PRIOR PLILING DATE: 2000-04-25
PRIOR PLILING DATE: 2000-04-25
PRIOR PLILING DATE: 2000-01-6
PRIOR FILING DATE: 1099-09-09/370,265
PRIOR FILING DATE: 1099-09-09/370,265
PRIOR PLILING DATE: 1999-07-09
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APPLICANT: Mulero, Julio
APPLICANT: Yeung, George
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US-09-608-285A-26
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Best Local Similarity:
Query Match:
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616 CGGGAACTACTGGTTGCTAAACGGACATTCCGTTCTGGAAGGCCACCCCT 675 130 LeuLysLeuGlyAlaThralaGlyLeuArgLeuLeuAspGlyAspAlaAlaGluLysle 149 130 LeuLysLeuGlyAlaThralaGlyLeuArgLeuLeuAspGlyAspAlaAlaGluLysle 149 140 LeuGlaAlaValArgGluMetPheArgAsnArgSerSerLeuSerValGlnProAspAla 169 150 LeuGlnAlaValArgGluMetPheArgAsnArgSerSerLeuSerValGlnProAspAla 169 170 ValSerValIleAspGlyThrGlnGluGlySerTyrLeuTrpValThrValAsnTyrLeu 189 170 ValSerValIleAspGlyThrGlnGluGlySerTyrLeuTrpValThrValAsnTyrLeu 189 171 ValSerValIleAspGlyThrGlnGluGlySerTyrLeuTrpValThrValAsnTyrLeu 189 172 GTTTCCATCAGAACGGAACGAGTGAGGGGTTTCGCGGGGGATCACTCTGTG 852 173 GTTTCCATCAGAACGGAACGAGTGAGGGGTTTCGCGGGGGATCACTCTGTG 852 174 LeuGlyLysLeuGlyLysLysPheThrLysThrValGlyValIleAspLeuGlyGlyAla 209 175 LeuGlyLysLeuGlyLysLysPheThrLysThrValGlyValIleAspLeuGlyGlyAla 209 176 LeuGlyLysCaGGAACCTCAAAACTCCAGGGGGACGAACTTGGCCGGACGA 912	210 SerValGlnMetAlaTyrAlaValSerArgAsnThrAlaLysAsnAlaProLysProPro 22	1258 ACGGAGGAAGTGAAGCAT
435 Db 1524 Qy Qy Qy Qy Qy Qy Qy Qy Qy Qy Qy Qy Qy	6 A 6 A 6 A 6 A 6 A 6 A 6 A 6 A 6 A 6 A	2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
416 GlyLeuAspProGluGluIleThrValAlaGluGlyIleGluTyrGlnAspAlaIle	FILE REFERENCE: 2810/36570 CURRENT APPLICATION NUMBER: US/09/608,285A CURRENT APPLICATION NUMBER: US/09/608,285A CURRENT FILING DATE: 2000-66-30 PRIOR PELICATION NUMBER: 09/583,231 PRIOR FILING DATE: 2000-06-26 PRIOR FILING DATE: 2000-04-25 PRIOR FILING DATE: 2000-04-25 PRIOR FILING DATE: 2000-04-25 PRIOR FILING DATE: 2000-04-25 PRIOR FILING DATE: 2000-04-21 PRIOR FILING DATE: 1099-08-09/310,265 PRIOR FILING DATE: 1999-08-09/310,265 PRIOR FILING DATE: 1999-07-09 PRIOR FILING DATE: 1999-07-09 PRIOR FILING DATE: 1999-07-09 PRIOR FILING DATE: 1999-07-09 PRIOR FILING DATE: 1999-07-09 PRIOR APPLICATION NUMBER: 09/273,447 PRIOR FILING DATE: 1999-07-09 PRIOR APPLICATION NUMBER: 09/122,449 PRIOR APPLICATION NUMBER: 09/122,449 PRIOR APPLICATION NUMBER: 09/122,449 PRIOR APPLICATION NUMBER: 09/118,205 PRIOR APPLICATION NUMBER: 09/118,205 PRIOR APPLICATION NUMBER: 09/118,205 PRIOR APPLICATION NUMBER: 09/118,205 PRIOR APPLICATION NUMBER: 09/118,205 PRIOR APPLICATION NUMBER: 09/118,205 PRIOR APPLICATION NUMBER: 09/118,205 PRIOR APPLICATION NUMBER: 09/118,205 PRIOR APPLICATION NUMBER: 09/118,205 PRIOR APPLICATION NUMBER: 09/118,205 PRIOR APPLICATION NUMBER: 09/118,205 PRIOR APPLICATION NUMBER: 09/118,205 PRIOR APPLICATION NUMBER: 09/118,205 PRIOR APPLICATION NUMBER: 09/118,205 PRIOR APPLICATION NUMBER: 09/118,205	27.62 A Homo sapiens E: Homo sapiens 550.00 Matches:
Cy Db Dy Cy Cy SEGULT RESULT RESULT GENE GENE GENE GENE GENE GENE TITT TITT	CURREN CURREN PRIOR PRIO	; SEQ ID NO ; TYPE: DN US-09-608-28 Alignment Sc Pred. No.; Score: Percent Simi Best Local S Query Match: DB: US-09-657-63 Qy 7 Oy 7 Db 51 Oy 7

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1018 TCCTACAGCTACCTCGGGCTCGGGCTGATGTCGGCACGCCTGGCGATCCTGGGCGCGTG 1077
                                                                     1078 gagddgcagccrgcraaggarggaaaggagrrggrcagccridcrigrcrccagrrrc 1137
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                                                                                                         282 GluAspileTyrArgTyrSerGlyGluSerTyrAsnileTyrGlyProThrSerGlyAla
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                                     -AlaAlaSerProCysLeuLeuAlaGlyTyr
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APPLICANT: Ford, John
TITLE OF INVENTION:
TITLE OF INVENTION: POLYPEPTIDES
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CURRENT FILING DATE: 1999-08-09
EARLIER APPLICATION NUMBER: PCT/US99/16180
EARLIER FILING DATE: 1999-07-06
EARLIER FILING DATE: 1999-07-09
EARLIER FILING DATE: 1999-07-09
EARLIER FILING DATE: 1999-03-19
EARLIER FILING DATE: 1999-03-19
EARLIER FILING DATE: 1999-03-19
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EARLIER FILING DATE: 1999-03-04
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EARLIER FILING DATE: 1998-07-16
NUMBER OF SEQ ID NOS: 37
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; Patent No. 644771
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913 TCCACTCAGATCGCCTTC---CTGCCACGCGTGGAGGCCACCCTGCAGGCCTCCCCACCC
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                                                              APPLICANT: Chadwick, Brian Paul
APPLICANT: Chadwick, Anna-Maria
TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE
TITLE OF INVENTION: POLYPEPTIDES AND NUCLEIC ACIDS
FILE REFERENCE: 9598-066
CURRENT APPLICATION NUMBER: US/09/240,639
CURRENT FILING DATE: 1998-01-29
NUMBER OF SEQ ID NOS: 29
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       Sequence 1, Application US/09240639
Patent No. 6350447
GENERAL INFORMATION:
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J Sequence 26, Application US/09557800C

Patent No. 6476211

GENERAL INCOMATION:

APPLICANT: Ford, John

APPLICANT: Ford, John

APPLICANT: Ford, John

APPLICANT: Ford, John

TITLE OF INVENTION: Methods and Materials Relating to CD39-Like

TITLE OF INVENTION: Methods and Materials Relating to CD39-Like

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FRICH RELING DATE: 2000-04-25

PRIOR PILING DATE: 2000-01-11

PRIOR PILING DATE: 1999-00-16

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APPLICANT: Ford, John
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APPLICANT: Ford, John
APPLICANT: Mulero, Julio
APPLICANT: Wedero, Julio
APPLICANT: Yeung, George
TITLE OF INVENTION: Methods and Materials Relating to CD39-Like
TITLE OF INVENTION: Methods and Materials Relating to CD39-Like
TITLE OF INVENTION: Moner: US/09/557,800C
CURRENT APPLICATION NUMBER: US/09/557,800C
CURRENT APPLICATION NUMBER: US/09/557,800C
PRIOR PILING DATE: 1999-00-0-11
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Fatent No. 6600032
GENERAL INFORMATION:
APPLICANT: Ford, John
APPLICANT: Milero, Julio
ITILE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39;
FILE REFERENCE: 28110/35908
CURRENT APPLICATION NUMBER: US/09/370,625A
CURRENT PILING DATE: 1999-00-09;
PRIOR APPLICATION NUMBER: PCT/US99/16180
FRIOR APPLICATION NUMBER: 09/350,836
FRIOR APPLICATION NUMBER: 09/273,447
FRIOR APPLICATION NUMBER: 09/273,447
FRIOR FILING DATE: 1999-03-19
NUMBER OF SEQ ID NOS: 39
SOFTWARE PALENT OF SEQ ID NOS: 39
SOFTWARE PALENT OF SEQ ID NOS: 39
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Mismatches:
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          PRIOR APPLICATION NUMBER: 09/244,444
PRIOR FILING DATE: 1999-02-04
PRIOR FULING DATE: 1998-07-24
PRIOR PRILING DATE: 1998-07-24
PRIOR FILING DATE: 1998-07-16
PRIOR FILING DATE: 1998-07-16
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PATCHTIN VEY: 2.0
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32.73%
21.01%
 1999-03-19
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                                                                                                                                                                                                                                                   Percent Similarity:
Best Local Similarity:
FILING DATE:
                                                                                                                                                                                                             Alignment Scores:
                                                                                                                                                                                 US-09-608-285A-54
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                                                            1018 TCCTACAGCTACCTCGGGCTCATGTCGGCACGCCTGGCGATCCTGGGCGGCGTG
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                                                                                                  ---AlaAlaSerProCysLeuLeuAlaGlyTyr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Ford, John
APPLICANT: Mulero, Julio
APPLICANT: Yeung, George
APPLICANT: Yeung, George
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CD39-LIKE
TITLE OF INVENTION: POLYPEPTIDES
FILE REFERENCE: 28110/36570
                                                                                                                                                                                                                                                                                                                                                                                                                                                               1387 TACGTGTGTCGGACCCTGGAGACACAGCCGCAGAGCAGC-----
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CURRENT APPLICATION NUMBER: US/09/608,285A
CURRENT FILING DATE: 2000-06-30
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PRIOR APPLICATION NUMBER: 09/583,231
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-04-25
PRIOR FILING DATE: 2000-04-25
PRIOR FILING DATE: 2000-01-11
PRIOR APPLICATION NUMBER: 09/481,238
PRIOR FILING DATE: 1999-08-09
PRIOR FILING DATE: 1999-08-09
PRIOR FILING DATE: 1999-09-06
PRIOR FILING DATE: 1999-09-08-09
PRIOR APPLICATION NUMBER: PCI/US99/1618(
PRIOR PRIOR DATE: 1999-07-06
PRIOR APPLICATION NUMBER: 09/350,836
PRIOR FILING DATE: 1999-07-09
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3ER: 09/583,231
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                                                                                                       270 AspGly----
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GENERAL INFORMATION:
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                                                                                                                                                 90 LysileLysProGlyLeuSerSerTyrAlaAspLysProGluLysAlaAlaGluSerLeu 109
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282 GluAspIl ::: 138 AAAGGAGA 302 AsnPheAs ::: 198 AGCCTGCA	316 LeuAsnGl 258 ACGGAGGA 336 Gly 318 GGTGTGGG	S Thrseral B AAAGATCA 7PheVa :: B CAGTTCCT	373 AlahlaLy 498 GCAGCCAA 393 GluLysAs, 546 413 AspGlyPh 588 CAGGAGTT 433 AspAlall.	
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Sequence 8688, Ap Sequence 2234, Ap

Title: Perfect score:

Sequence:

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Scoring table:

Minimum DB Maximum DB

Searched:

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Sequence 1, Application US/09129112
Batent No. US2002001995A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Etzler, Marilynn E.
APPLICANT: He Regents of the University of California
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: A No. US20020019995A1 Factor Binding Protein From Legume Roots
FILE REFERENCE: 023070-07981UUS
CURRENT APPLICATION NUMBER: US/09/129,112
CURRENT FILING DATE: 1999-08-04
PRIOR APPLICATION NUMBER: US 08/907,226
NUMBER OF SEQ ID NOS: 19
SOFTWARE: Patentin Ver. 2.1
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18: /cgn2_6/ptodata/2/pubpna/US10_NEW PUB.seq:*
19: /cgn2_6/ptodata/2/pubpna/US10_NEW PUB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                              - nucleic search, using frame_plus_p2n model
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                                                                                                                                                                                                                                                                                                                                                                                                                3228839 seqs, 2456066551 residues
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Maximum Match 1008
Listing first 45 summaries
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7.0
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Ygapop 10.0 , Ygapext
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Database

Sequence Sequence 2

Description

Query Score Match Length DB

Sequence

Sequence Sequence

Sequence Sequence Sequence

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of California
Factor Binding Protein From Legume Roots
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                                             TCCCATGAAAACTGCACCTTTGGTGGGGATATGGGATGGTGGAAAAGGAAGTGGACAGAAA 1070
                                                                                                                                                            1071 AACCTIGITGITACTICAGCTITCIACIATAGGICTICIGAGGITGGTITTGICACTCCT 1130
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TATGAAGATATATACAGATATTCCGGAGAATCGTACAATATCTATGGTCCCACTTCTGGT 950
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                             AlaAsnPheAsnGluCysArgAspLeuAlaLeuGInIleLeuArgLeuAsnGluProCys
                                                                                 SerHisGluAsnCysThrPheGlyGlyIleTrpAspGlyGlyLysGlySerGlyGlnLys
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Fatent No. US20020019995A1
GENERAL INFORMATION:
APPLICANT: Etaler, Marilynn E.
APPLICANT: Murphy, Judith B.
APPLICANT: THE REGENTS of the University of
TILE REFERENCE: 02070-079810US
CURRENT APPLICATION NUMBER: US/09/129,112
CURRENT FILING DATE: 1998-08-04
PRIOR APPLICATION NUMBER: US 08/907,226
FILING DATE: 1997-08-06
NUMBER OF SEQ ID NOS: 19
SOFTWARE: Patentin Ver. 2.1
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OTHER INFORMATION: genomic
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; OTHER INFORMATION: NBP46 (DB46) No. US20020019995A1 factor binding lectin; NAME/KEY: mat_peptide; LOCATION: (195)..(1436)
US-09-129-112-1
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Conservative:
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Indels:
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in a company of the c	(1698).	.777-	6.29e-211 Length: 1741 00 Marches:	milarity: 29.01% Conservative: Similarity: 29.01% Mismatches:	72.42% Indels: 9 Gabs:	31-2 (1-462) x US-09-129-112-3 (1-6265)	MetAsnTrpValTrpProLysThrLysSerMetSerPheLeuLeuLeulFill=ThrPheLeu	5 AIGAAITGGGGGGGGAAAGACAAAGAGCAIGAGCTICCTACTCCTCATCACTTTCTA	1 LeuPheSerLeuProLysLeuSerSerSerGlnTyrValGlyAsnSerIleLeuLeuAsn	s ciciicicalisccaaaaciiiciiciicgcaaigiiggggaaCaGTACTAAAAT	HISATQUYSILELEUKTOASNGINGLULEULEUTTSETTYTALAVAIITEPIRASPALA HINTIN HI	GlySerSerGlySerArgValHisValPheAsnPheAspGlnAsnLeuAspLeuLeuHis		1 IleGlyAsnAspLeuGluPheThrLysLys		Jensey Tille	TATITICITCATCTTACTTTACAITCTTCTTCAITATICIGGIGCAGAICAAACCCGGT	95 LeuSerSerTyrAlaAspLysProGluLysAlaAlaGluSerLeulleProLeuLeuGlu	035 TTGAGCTCATACGCTGATAAGCCTGAAAAGCTGCAGAATCTCTCATTCCACTTTTGGAG	115 GludaGludssyalValProGluGludeuHisProLysThrProLeuLysLeuGly	133	5 AGTATITCTCATCTCTACTITTGCCACAGATTAATATGTCACACTTTTACATGAAACATG	3	ATTAAGTTCTTTAAACATGTTGATTAAAGGGTGACAGTTTGTATTTTTAATCAAGTAAT	3	275 CTAGBACTTABAACTAIGGTABIATABABATGABIATGBAACTBATATATTCTGAIGGA	3	5 ACAGAAGAAAGCAATATCAAGAGAGACAAAACACACACTTTGATGAGGCTCTATCTTTTAA	33	95 ACAAAAAATGGAATTGAAAGACCAAATAAAATAGGCATTAGCCCATATCATAAAATCTTT	3	5 TGTAAAATTATTAATAGAAAGTAAATGAACACTATATATA	4AlaThrAlaGlyLeu	

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ArgLeuLeuAspGlyAspAlaAlaGluLysIleLeuGlnAl. 		CATTICCTIAIGITATIAACTACGCTITCAA	ValArgGluMetPheArgAsnArgSerSerLeuSerVa- 		VALILEASPOLYINGINGINGINGSTYLING CHIATTGATGGAACCCAAGAAGGTTCTTACTT		TTTATCAGAATTCATTCTAATTTTTTACT		ACCTAGGACATTCATCTTATTTAAAATAAT		GAATTGATATTTGCGTATATTGTGAAAAG		GTATTTTAATAAATTTTTATTAACTCTTTTTAA		GTGTGTGGTGACATGCCATACCCCATATGG		TAATATTTTATCAATTGTCAATTTATTTATTGTAACTA		AATCATTGAGGTATCGCTTTAGTTTTTTTTTAAAT		GATATACTGGAAGAATTTCCGAAGGATATTC		TTTTTATTGAACAAATGCAACACTATCTCTF		ATCACGACGATATAATTTTGTATAAGTAATT		TITCTITIAGGGTCCGCCAATTAGCTAAATC		aagaaagaagcaatgatgaaattaaaagtgga <i>t</i>		AAGAATTAGGTTCTTTGTTATGTTTTCAAAAA		TATAATTATTAATAAAATTGTCTGCTTAAT	
139	152	1635	153	, ,	1755	184	1814	184	1874	184	1934	184	1994	184	2054	184	2114	184	2174	184	2234	184	2294	184	2354	184	2414	184	2474	184	2534	184	2594	5
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3734 AGGCATAAATTGTTCTCGAAATTAGTTATATTTTGTTCAATTTTAACAAAATCATCTCA	QY 251	251	Db 3854 GTACAAACCTAAAAGGTGTTTCTTTTTTTTTAATTTGAAGAACTAGAATATTGTTTTT 3913		Э	Db 3974 TTATAACGAATGTCACAAAAAAAAGGTAGGTAGGTATGTTATAAATACTTCTGATATCAAAATGG 4033	251	Db 4034 CAAAAACTCCAGAGTCTCCAAGAATCATCATCATTTTTTTCTCACCTTAATCTGAAATA 4093	Δy 251 251 Db 4094 ATGAATGCTTACTTTTTTAAGATATTTATAGATATCTATAATCCATTGAAGTTCAGTGT 4153	251	4	Db 4214 TTTTTARGGTTTAAACTGATAAAATATGCGTGATGATGATGATGATGATGATGATGATGATGATGATGA	Oy 252SerTyrLeuArgTyrGlyAsnAspAlaAlaAlaArgVallySle 265	266	Db 4334 TTTAAGACCACTGGTGGTGCTGCTGCCTGCCTATTGGCAGGCTATGAAGTAATAA 4393	282	Db 4394 AGTATTCTTTGTACAACCCTAATGTTACTTCTTATTCCTGCATTCAGAATAGTGCAA 343.	202 4454 AGGACTGAAACTAGAAAGGATTCCAATTCACTACAAGAAAAAAAA	282	Db 4514 TGACCAAAGTTACTTTTTCCTCACTGAGTTCTATTGAAATGCAGAAACTTGTTGCAGATA 4573	282	DB 4574 TITIAAAIACAIATTAAGTGTTTGTCAGTACTGCATITGTTTTAGTGATTTCAGTGTGTTTGTCAGTGTGTTTAGTGTGTTTTGTTTTAGTGTGTTGTTTTAGTGTGTTGT	4	283	Db 4694 GATATATACAGATATTCCGGAGAATCGTACAATATCTATGGTCCCACTTCTGGTGCCAAC 4753		
654 TTTRABARTHATATTTTAAATTTATTTTTATTTTAGATAAATTTTGGT 2713	84	2714 AATATTTATAATATTTTAAATTAAATTTCAAACTTGTTGTGATCTTACTTA		2774 ATTATTTTTTCAGTTTTCAATTATTGCATTTTTTTTTTT	184		2894 TATCTGCATTATGTTTATTTGAATAGTAAAACACTATAAAATATATGTTAATGTAAAGGAT 2953		2954 AAACAIGCAGAGTAGTAAAAACTTATTAGAATATAGTCATTTATTT	3014 TATCTTGGGAATTTTGTGTAGGTTACAGTTAACTATCTTTAGGAAAAGTTGGGAAAGAAG 3073	197 PheThriysThrValGlyVallleAspLeuGlyGlyAlaSerValGlnMetAlaTyrAla 216	ValSerArgAsnThrAlaLysAsnAlaProLysProFroGlnGlyGluAspProTyrMet	3134 GTCTCAAGAAATACAGCTAAAAATGCCCCCAAAACCCCCACAAGGAGGAGGATCCATACATG 3193 237 LystysLeuvalleulysGlylysLysTyrAspleuTyrValHis 251	3194 AAGAAGCTIGIACTCAAGGGAAAGAAATATGACCTITATGTICACAGGTIACTTICTGTT 3253	251		3314 TAAAATCAAATAACATAAAAAATGGTAATATAATGTTGCGTTTTGGGAFTGTTTGGATT 3373	251 251	3374 aaagggtaaatttgaagaagaaaaaataataataaataa	251		3494 TITAATTATTTATTATTAAAAATAAAATATTTATTTTAAATTTT	251 251	3554 TITITAATITITAATTATTAAAAATATAATATTATTAATAA		3614 TTTATTAATATAATAATAATAAATAAATAAATAATAATA	3674 TITAAITATACAIATGIAITTITTITCIGCAAAITTITACCTITITAAGCGGAGAAGAIGA 3733

Percent Similarity: 83.05% Conservative: 68 Best Local Similarity: 68.45% Mismatches: 71 Query Match: 70.05% Indels: 8 DB: 5	US-09-657-631-2 (1-462) x US-09-129-112-13 (1-1489)	alTrpProLysT	25	OY 20 LeuLeuPheSerLeuProLysLeuSerSerGlnTyrValGlyAsnSerIleLeuLeu 39 ::: ::	Oy 40 AsnHisArgLysIleLeuProAsnGlnGluLeuLeuThrSerTyrAlaValIlePhe 58	59 AspA		Oy 79 LeuHisIleGlyAsnAspLeuGluPheThrLysLysIleLysProGlyLeuSerSerTyr 98		313 GCTGCTAATCCTGAAGAAGCTGCAGAATCTCTGATTCCACTTCTAAAAGAAGCAGAAAT	OY 119 ValvalProGluGluLewHisProLygThrProLeuLysLeuGlyAlaThrAlaGlyLeu 138	139 ArgLeuLeuAspGlyAspAlaAlaGluLysIleLeuGlnAlaValArgGluMetPheArg	433 AGGCTTTTGGAGGGGAATGCTGCTGAAAATATTGCAAGCGGTCAGGGATATGCTCAGC 49	LDS ASHAGGSETSELENDENTALGINFOASDALAVAISETVALGINGIU 178 LDA ASHAGGAAGGGCCCTTAATGTTCAATCAGATGCAGTATCTATTCTTGATGGAACCCAAGAA 552	Oy 179 GlySerTyrLeuTrpValThrValAsnTyrLeuLeuGlyLysLeuGlyLysLysDheThr 198	Qy 199 LysThrValGlyValIleAspLeuGlyGlyAlaSerValGlnMetAlaTyrAlaValSer 218	Qy 219 ArgAsnThrAlaLysAsnAlaProLysProProGlnGlyGluAspProTyrMetLysLys 238	Qy 239 LeuValleuLysGlyLysLysTyrAspLeuTyrValHisSerTyrLeuArgTyrGlyAsn 258	n 27	793	Qy 279 AladlyTyrGluAspIleTyrArgTyrSerGlyGluSerTyrAsnIleTyrGlyProThr 298	Qy 299 SerGlyAlaAsnPheAsnGluCysArgAspLeuAlaLeuGlnIleLeuArgLeuAsnGlu 318	319 P
Qy 343 ValvalThrSerAlaPheTyrTyrArgSerSerGlu	Qy 354 354	4934 GTTTACTTTGATTACTTATT	9	368 LeuaspPheGluThrAlaAlaLysGlndlaCysSerLeuThrPheGluGluAla	Db 5054 CTGGATTTTGAAACTGCAGCTAAACAAGCTTGTTTTAACATTGGAGGAAGCGAAATCC 5113 Qy 388 ThrPheProAsnValGluLvsAspLvsLeuProPheValCvsValasnPheThyrgln 407	5114 ACTITICCAAAIGITGAGAAAGAIAAACTICCAITIGIALIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	408 TyrThrLeuLeuValAspGlyPhe41	DD 51/4 IAIACATTGCTTGATGGATTTGGTATTTCATAATTACCAAGTTGATATT 5233 QY 415415	Db 5234 AACTICTTCCAAAAACTATGTTTTCTTTTGTCTTCCAACACTGACTCCTAAITCAACTT 5293	43	434	5354 GCCATTGTGGAAACAGCATGGCTCTAC	27		Sequence 13, Application US/09129112 ; Patent No. US20020019955A1 ; GENERAL INFORMATION : A DPLICANT FF-10-Y MARILUME	APPLICANT: Murphy, Judith B.; APPLICANT: The Regents of the University of California TYNENTION: A NO. US20020019995Al Factor Binding Protein From Legume Roots FILE DF PERFERENCE: 073070_07001001	CURRENT APPLICATION NUMBER: US/09/129,112 ; CURRENT FILING DATE: 1998-08-04 ; PRIOR APPLICATION NUMBER: US 08/907,226 ; PRIOR FILING DATE: 1008/907,226		TYPE: DNA : TYPE: DNA : GRANISM: Lotus japonicus	FEATURE: 1 TOCART/FOR (1) (1400)	RMA CDS (43	; OTHER INFORMATION: NBP46 US-09-129-112-13	Alignment Scores: Pred. No.: 1.12e-204 Length: 1489 Score: 1684.00 Matches: 319

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AsnArgProLeuAspPheGluThrAlaAlaLysGlnAlaCysSerLeuThrPheGluGlu 384
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                                                                                                                                                              TIGITGACAAGAICAAACCAGGITIGAGIGCAIAIGGGGGAIAAICCIGAACAAGCAGCA 303
                                                                                                                                                                                                                                                                      AAATCTCTCATTCCACTTTTGGAGGAGAAGCAGAAGATGTGGTTCCTGAGGATCTCCGACCC 363
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67 ATCACTTCCTCCCAATATTTAGGAAACAACCTACTCACTAAT---CGAAAGATTTCCAA
                                                                                           47 AsnGlnGluLeuLeuThrSerTyrAlaValIlePheAspAlaGlySerSerGlySerArg
                                                                                                                                               ValHisValPheAsnPheAspGlnAsnLeuAspLeuLeuHisIleGlyAsnAspLeuGlu
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                                     LeuSerSerGlnTyrValGlyAsnSerIleLeuLeuAsnHisArgLysIleLeuPro
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RAPPLICANT: ETZIEr, Marilynn E.

APPLICANT: Etzler, Marilynn E.

APPLICANT: The Regents of the University of California

TITLE OF INVENTION: A No. USZU0ZO019995A1 Factor Binding Protein From Legume Roots

FILE REPERENCE: 023070-079810US

CURRENT APPLICATION NUMBER: US/09/129,112

CURRENT FILING DATE: 1998-08-04

PRIOR APPLICATION NUMBER: US 08/907,226

PRIOR APPLICATION NUMBER: US 08/907,226

NUMBER OF SEQ ID NOS: 19

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 8
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                                                                                                                                                                                                                                                                                                                   GAAGCCGCATGGCCTCTAGGCCACTGCCATAGAAGCAATATCATTGCTAAATTTGAG 1392
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                                                                                                                                                      GluThrAlaTrpProLeuGlyThrAlaIleGluAlaIleSerSerLeuProLysPheAsn 456
                                                                                 ValThrProProAsnSerLysAsnArgProLeuAspPheGluThrAlaAlaLysGlnAla 377
                                                                                                                                        CysSerLeuThrPheGluGluAlaLysSerThrPheProAsnVal ---GluLysAspLys 396
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                                                                                                  CCTTGTCCCTATCAGAATTGCACTTTTGGTGGGATATGGAATGGTGGAGGTGGAAGTGGT
                                GlnLysAsnLeuValValThrSerAlaPheTyrTyrArgSerSerGluValGly---Phe
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965 GGGATATGGAACGGTGGAGGGGGAGTGGACAAAAAGTCCTTTATGTTACTACATCTTTC 1024
                    ProLeuLysLeuGlyAlaThrAlaGlyLeuArgLeuLeuAspGlyAspAlaAlaGluLys 148
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                                                                    IleLeuGlnAlaValArgGluMetPheArgAsnArgSerSerLeuSerValGlnProAsp
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Publication No. US2004003488A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Edou, Yihua
APPLICANT: Evoalic, David K.
APPLICANT: Acven E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: TOGO, YORGWei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILLE REFRENCE: 38-21(531313)
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT APPLICATION NUMBER: US/10/425,114
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 8688
CTTCATCCAGTAGATTTCGAAATTGAAGCTAAGCGAGCTTGTGCATTAAACTTTGAGGAT 1143
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                                     ThrTyrGlnTyrThrLeuLeuValAspGlyPheGlyLeuAspProGluGlnGluIleThr
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Matches:
Conservative:
Mismatches:
Indels:
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US-10-425-114-8688
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Query Match:
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Sequence 11000. US2004003488BA1
Sequence 11000. US2004003488BA1
Septicant: Lin, Jingdong
APPLICANT: Edou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: APPLICANT: Applicant Serven E
APPLICANT: Gao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFRENCE: 38-21(53113)B
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
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                                             ProGlnGlyGluAspProTyrMetLysLevSleuValLeuLysGlyLysLysTyrAspLeu
                                                               LeualaLeuGlnIleLeuargLeuasnGluProCysSerHisGluAsnCysThrPheGly
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US-10-425-114-11084
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                                                           APPLICANT: LOSG Thomas J
APPLICANT: Kovalic David K
APPLICANT: Thou Yihua
APPLICANT: Thou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERRNCE: 38-21(3)223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT APPLICATION NUMBER: US/10/424,599
SEQ ID NOS: 285684
SEQ ID NO 2234
                                                                                                                                                                                                                                                                                                                                                         1532
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Conservative:
Mismatches:
Indels:
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                      Sequence 2234, Application US/10424599 Publication No. US20040031072A1 GENERAL INFORMATION:
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ORGANISM: Glycine max
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NAME/KEY: primer bind
LOCATION: Complement (1)...(22))
OTHER INFORMATION: DEXCOP primer
NAME/KEY: primer bind
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LOCATION: (61)..(1404)
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Matches:
Conservative:
Mismatches:
Indels:
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; OTHER INFORMATION: Clone ID: 701006212_FLI
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US-09-129-112-18
Sequence 18, Application US/09129112
Patent No. US20020019995A1
Sequence 18, Application US/09129112
Sequence 18, Application US/09129112
Sequence 18, Application Sequence 18, Application Murphy, Judith B.
APPLICANT: Harby, Judith B.
TITLE OF INVENTION: A No. US20020019995A1 Factor Binding Protein From Legume Roots FILE REPRENCE: 220700-099810US
CURRENT APPLICATION NUMBER: US/09/129,112
PRIOR PLILNG DATE: 1998-08-04
NUMBER: US/08/907,226
NUMBER OF SEQ ID NOS: 19
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1319 CTCGTGGAAGCAGCATGGCCACTAGAGGCCATAGAAGCCATATCATTACCTAAA 1378
                         AsnGluProCysSerHisGluAsnCysThrPheGlyGlyIleTrpAspGlyGlyLysGly 336
ProThrSerGlyAlaAsnPheAsnGluCysArgAspLeuAlaLeuGlnIleLeuArgLeu 316
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1139 AAGTTGCCTGTAACACAGAATTAAAGGATCTCAAATCCATTTTCCCTCGTGTTAAGGAT
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OTHER INFORMATION: DBX gene involved in oligosaccharide signaling
NAME/KEY: sig_peptide
NAME/KEY: (60)
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OTHER INFORMATION: DEX8 primer
NAME/KEY: primer bind
LOCATION: (297)...(314)
OTHER INFORMATION: DEX7-for/rev primer
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: (1133)...(1151)
OTHER INFORMATION: DBX9-for/rev primer
NAME/KEY: primer_bind
LOCATION: (1227)...(1247)
OTHER INFORMATION: DBX12 primer
NAME/KEY: primer_bind
LOCATION: (1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)...(1414)
           NAME/KEY: primer_bind
LOCATION: (667) -. (685)
OTHER INFORMATION: DBAL-for/rev primer
NAME/KEY: primer_bind
                                                                                                          primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: Complement ((1075)..(1093))
OTHER INFORMATION: DEX11 primer
NAME/KEX: primer_bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ) OTHER INFORMATION: DEXBottom primer US-09-129-112-18
                                                                                    LOCATION: [688). (704)
OTHER INFORMATION: DBX2-for/rev pr.
NAME/KEY: primer_bind
LOCATION: Complement (766). (785)
OTHER INFORMATION: DBX10 primer
                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: (955). (972)
OTHER INFORMATION: DBX4 primer
NAME/KRY: misc feature
LOCATION: (1071). (1072)
OTHER INFORMATION: splice site
NAME/KRY: primer_bind
                                                                                                                                                                                                  LOCATION: (856)..(857)
OTHER INFORMATION: splice site
NAME/KEY: primer_bind
LOCATION: (857)..(872)
                                                                                                                                                                                                                                                   OTHER INFORMATION: DBX5 primer NAME/KEY: primer bind LOCATION: (933)...(952) OTHER INFORMATION: DBX3 primer NAME/KEY: primer_bind
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1341.50
73.72%
54.49%
55.80%
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LOCATION: (856). (857)
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APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joe1
APPLICANT: Kreps, Joe1
APPLICANT: Wang, Xun
APPLICANT: ALL
APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REPERENCE: SCRIP1300-3
CURRENT FILING DATE: 2001-08-24
PRIOR PPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
                                                                                                                                                   1301 GGCTGGTTTTTGTTGATCCAAACGCCCCAAAGTTCGTCCTGTGGGATTTTGAG 1360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1361 AATGCAGCAAAGGTTGCCTGTAACACAGAATTAAAGGATCTCAAATCCATTTTCCCTCGT 1420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              335 ysglySerglyGlnLys-AsnLeuValValThrSerAlaPheTyrTyrArgSerSerGlu 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           372 ThrAlaAlaLysGlnAlaCysSerLeuThrPheGluGluAlaLysSerThrPheProAsn 391
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                  AlaValSerArgAsnThrAlaLysAsnAlaProLysProProGlnGlyGluAspProTyr
LysPheThrLysThrValGlyValIleAspLeuGlyGlyAlaSerValGlnMetAlaTyr
                                                                                                                            236 MetLysLysLeuValleuLysG]yLyslysTyrAspLeuTyrValHisSerTyrLeuArg
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1061 TGTATTTTGGCTGGCTTTTGATGGGTATTACGTATATGGAGGAGTGCAGTATAAGGCCAAA
                                                                                                                                                                                                                                                                                                                          296 GlyProThrSerGlyAlaAsnPheAsnGluCysArgAsp-LeuAlaLeuGlnIleLeuAr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               355 ValGlyPheVal-----ThrProProAsnSerLysAsnArgProLeuAspPheGlu
                                                                                                                                                                                             TyrGlyAsnAspAlaAlaArgValLysIlePheLysThrThrAspGlyAlaAlaSerPro
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584 GCAGAAGCTGCTGTTCCTCAGGAGTTTCACCCCAGGACGCCAGTTAAACTTGGAGCAACT
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                 Sequence 87316, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: LA ROSA Thomas J
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement;
FILE REFRENCE: 38 = 21 (5323) B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24 LeuProLysLeuSerSerGlnTyrValGlyAsnSerIleLeuLeu
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                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Clone ID: PAT_MRT3847_49857C.1
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Matches:
Conservative:
Mismatches:
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1292.00
72.30%
53.91%
                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity:
Query Match:
     US-10-424-599-87316
                                                                                                                                                                                                                                                                                                                                   US-10-424-599-87316
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                                                                                                                                                                                                                                   SEQ ID NO 87316
LENGTH: 1784
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APPLICANT: Harper, Jeff
APPLICANT: Wang, Xun
APPLICANT: Wang, Xun
APPLICANT: Wang, Xun
APPLICANT: Wang, Xun
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
TITLE OF INVENTION: SAME, AND METHODS OF USE
TITLE OF INVENTION: SAME, AND METHODS OF USE
TITLE OF INVENTION: SAME, AND METHODS OF USE
TITLE OF INVENTION: SAME, AND METHODS OF USE
TITLE OF INVENTION NUMBER: US 60/2938,842A
CURRENT FILING DATE: 2001-08-24
PRIOR FILING DATE: 2000-08-24
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
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                                                                                                                                                                                                                                                                                                                                                                                                                    LeuvalaspGlyPheGlyLeuAspProGluGlnGluIleThrvalAlaGluGlyIleGlu 430
                                                                                                                                                                             GlyGlyLysGlySerGlyGlnLysAsnLeuValValThrSerAlaPheTyrTyrArgSer 352
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                 GCCCTGCTTCACAATCGGGTGCGAGTCTTGACGAGTGCCGAAGGATAACCATCAACGCA
                                                                                                                                                                                                                                       SerGluValGlyPheValThrPro-----ProAsnSerLysAsnArgProLeuAspPhe
                                                                                                                                                                                                                                                        274 SerproCysLeuLeuAlaGlyTyrGluAspIleTyrArgTyrSerGlyGluSerTyrAsn
                                                        294 IleTyrGlyProThrSerGlyAlaAsnPheAsnGluCysArgAspLeuAlaLeuGlnIle
                                                                                                                   | LeuArgLeuAsnGluPro---CysSerHisGluAsnCysThrPheGlyGlyIleTrpAsp
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana
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1281.50
74.15%
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Query Match:
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US-09-938-842A-1888
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LENGTH: 1419
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Mismatches:
Indels:
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      PRIOR APPLICATION NUMBER: US 60/264,647 PRIOR FILING DATE: 2001-01-16 PRIOR PULICATION NUMBER: US 60/300,111 PRIOR FILING DATE: 2001-06-22 NUMBER OF SEQ ID NOS: 5379
                                                                                                                                ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                     3.76e-153
1281.50
74.15%
54.88%
53.31%
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Best Local Similarity:
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US-09-938-842A-1888
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Pred. No.:
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LENGTH: 1419
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DB: US-09-657-631-2 (1-462) x US-09-938-842A-1888 (1-1419) QY 14 LeuLeuLeuleuleurherheleuLeurheserLeurproLysLeuSerSerGlnTyrval 33 ::::	211 271 94 331 114 114	OY 134 AlaThrAlaGlyLeuArgLeuLeuAspGlyAspAlaAlaGluLysIleLeuGlnAlaVal 153 451 GCTACTGCAGGTTTGAGGACGTGGTGATCTTGAGACATTTGCAAGCGGTT 510 Db 451 GCTACTGCAGGTTGAGAGCTCATGAGCATTTGCAAGCGGTT 510 OY 154 ArgGluMetPheArgAsnArgSerSerLeuSerValGlnProAspAlaValSerValIle 173 Db 511 AGGGAACTCCTGAGAGATGAGAAGCATGAAAACTGAAAAGCAAATGCTGTAACTGTACTG 570 OY 174 AspGlyThrGlnGluGlySerTyrLeuTrpValThrValAsnTyrLeuLeuGlyLysLeu 193 Db 571 GATGGTACCCAGGAAGTTCTTATCAGTGGGTAACAATTAACTACTGCTAAGGAACTTG 630 OY 194 GlyLysLysPheThrLysThrValIleAspLeuGlyGlyAlaSerValGlnMet 213 COA 195 GlyLysLysPheThrLysThrValGlyValIleAspLeuGlyGlyAlaSerValGlnMet 213 COA 196 GlyLysLysPheThrLysThrValGlyValIleAspLeuGlyGlyAlaSerValGlnMet 213	214 691 234 751 254	274 SerProCysLeubeuhlaGlyAyrGluAspIleTyrArgTyrSerGlyGluSerTyrAsn 293 371 AACCCCTGCATCGGGCGAGGCTATGATGAAGTATGGAGAAAAGAATTTAA 930 294 IleTyrGlyProThrSerGlyAlaAsnPheAsnGluCysArgAspLeuhlaLeuGlnIle 313 373 GCCCTGCTTCACAATCGGGGGTCTTGACGAGGTGCCGAAGGATAACCATCAAAGGA 374 LeuArgLeuAsnGluProCysSerHisGluAsnCysThrPheGlyGlylleTrpAsp 332

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APPLICANT: Kreps, Joel
APPLICANT: Kreps, Joel
APPLICANT: Thin, Tong
APPLICANT: And, Tong
APPLICANT: APA, TONG
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC FLANTS CONTAINING
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIPIA180-3
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2000-08-24
FRIOR APPLICATION NUMBER: US 60/227,866
FRIOR APPLICATION NUMBER: US 60/264,647
FRIOR APPLICATION NUMBER: US 60/300,111
FRIOR FILING DATE: 2001-06-22
FRIOR APPLICATION NUMBER: US 60/300,111
FRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 849
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                                                                                              US/09938842A
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1227.00
71.43%
53.51%
51.04%
                                                                                              ; Sequence 849, Application ; Patent No. US20020160378A1
                                                                                                                            GENERAL INFORMATION:
APPLICANT: Harper, Jeff
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Best Local Similarity:
Query Match:
DB:
                              1298 TCG 1300
Ser 451
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AGGGACATICTICGCGAAAAGAGTICCTITAAAACCAACCAGATICGGTIACAGTICTI 457
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                                   GluGluAlaGluAspValValProGluGluLeuHisProLysThrProLeuLysLeuGly
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                  GlyLeuSerSerTyrAlaAspLysProGluLysAlaAlaGluSerLeuIleProLeuLeu
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  CURRENT FILING DATE: 2001-08-24

PRIOR APPLICATION NUMBER: US 60/227,866

PRIOR FILING DATE: 2000-08-24

PRIOR FILING DATE: 2000-08-24

PRIOR FILING DATE: 2001-01-16

PRIOR APPLICATION NUMBER: US 60/264,647

PRIOR APPLICATION NUMBER: US 60/300,111

NUMBER OF SEQ ID NOS: 5379

SEQ ID NO 849

LENGTH: 1416
                                                                                                                                          TYPE: DNA
ORGANISM: Arabidopsis thaliana
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APPLICANT: Kreps, Joel
APPLICANT: Kreps, Joel
APPLICANT: Kreps, Joel
APPLICANT: Zhu, Tun
APPLICANT: Zhu, TORRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REPERENCE: SCRIP1300-3
CURRENT APPLICATION NUMBER: US/09/938, 842A
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868 AACCCTGTATCGCGACTGGATATGCTGGTACCTACAAATATGGAGGAAAAGCGTTTAAA
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Percent Similarity: 70.36% Conservative: 79 Best Local Similarity: 52.49% Mismatches: 117 Query Match: 49.54% Indels: 14 DB: 6aps: 5 US-09-657-631-2 (1-462) x US-10-437-963-29868 (1-2071)	Qy 14 LeuLeuLeulleThrPheLeuLeuPheSerLeuDroLysLeuSerSerGln 31	Qy 32 TyrValGlyAsnSerIleLeuLeuAsnHisArglySIleLeuPrcAsnGlnGluLeuLeu 51	Oy 52 ThrSerTyrAlaValllePheAspAlaGlySerSerGlySerArgValHisValPheAsn 71	Oy 72 PheaspdlnasnLeuAspLeuLeuHisIleGlyAsnAspLeuGluPheThxLysLysIle 91	Qy 92 LysProdlyLeuSerTyrAlaAspLysProdluLysAlaAlaGluSerLeuIlePro 111	Oy 112 LeuLeuGludluAladluAspValValProGluGluLeuHisProLysThrProLeuLys 131	Oy 132 LeuGlyAlaThrAlaGlyLeuArgLeuLeuAspGlyAspAlaAlaGluLysIleLeuGln 151 :::	OY 152 AlaValArgGluMetPhcArgAsnArgSerSerLeuSerValGlnProAspAlaValSer 171	Oy 172 ValileAspGlyThrGlnGluGlySerTyrLeuTrpValThrValAsnTyrLeuLeuGly 191	Qy 192 LysLeuGlyLysLysPheThrLysThrValGlyVallleAspLeuGlyGlyAlaSerVal 211	Oy 212 GluMetAlaTyrAlaValSerArgAsnThrAlaLysAsnAlaProLysProGlnGly 231	Qy 232 GluaspProTyrMetLysLysLeuValLeuLysGlyLysLysTyrAspLeuTyrValHis 251	Oy 252 SerTyrLeuArgTyrGlyAsnAspAlaAlaArgValLysIlePheLysThrThrAspGly 271	290	U	Qy 291 SerTyrAsnIleTyrGlyProThrSerGlyAlaAsnPheAsnGluCysArgAspLeuAla 310	Qy 311 LeuGlnIleLeuArgLeuAsnGluProCysSerHisGluAsnCysThrPheGlyGlyIle 330 :::::	Oy 331 TrpAspGlyGlyLySsGlySerGlyGlnLySASnLeuValValThrSerAlaPheTyrTyr 350
Db 808 CTACATTACGGGTTACTGGCTCGCGGCTGGATTTTGAAAGTTTCTGAGGACTCTAAC 867 Qy 274 SerProCysLeuleualaGlyTyrGluaspileTyrArgtysSerGlyGluseTyrAsn 293 Db 868 AACCCTGTATGGCGACTGGTGGTGCTGCTACAAATAGGAAGAAAAGGGTTAAA 927	294 IleTyrGlyProThrSerGlyAlaAsnPheAsnGluCysArgAspLeuAlaLeuGlnIle 928 GCTGCAGCTTCTCCATCCGTGCAACTCTAGATGAAGTGCCGAGTGACTATTAACGCA	314 988	333	353	371	391	Qy 411 LeuvalAspGlyDheGlyLeuAspProGluGlnGlulleThrValAlaGluGlyIleGlu 430	Qy 431 TyrGlnAspAlaIleValGluThrAlaTrpProLeuGlyThrAlaIleGluAlaIIleSer 450	451	SULT 15 -10-437-9 Semience	LOD INFO	н	Bark Li, IVENT	; FILE REFERENCE: 38-21(53221)B ; CURRENT APPLICATION NUMBER: 08/10/437,963 ; CTREDENT PITTAG DATE: 2003-06-14	CURRENT FILING DAIE: 2003-02-14; CURRENT FILING DAIE: 2004-05; MUMBER OF SEQ ID NOS: 2049-66	; SEQ ID NO 29868 ; LENGTH: 2071 ; TYPE: DNA	; FEATURE: ; CTHER INFORMATION: Clone ID: PAT_MRT4530_34328C.1 US-10-437-963-29868	Alignment Scores: 2.79e-141 Length: 2071 Pred. No.: 1191.00 Matches: 232

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-MODEL=frame+ p2n.model.-DEV=xlh
-MODEL=frame+ p2n.model.-DEV=xlh
-MODEL=frame+ p2n.model.-DEV=xlh
-DS=CB_CS_1/USFO_SPOOl/USO9657631/runat_10082004_171045_1674/app_query.fasta_1.1294
-DS=CB_CS_1/USFO_SPOOl/USO9657631/runat_10082004_171045_1674/app_query.fasta_1.1294
-DB=CGB_DS_1/USFO_SPOOL_PSOOL_PSOOL_NEVER_SED_0.TSG_NEVER_SED_0.TSG_NEVER_SED_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_NES_0.TSG_
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3589.832 Million cell updates/sec
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(c) 1993 - 2004 Compugen Ltd.
                                                                                                  - nucleic search, using frame_plus_p2n model
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3470272 seqs, 21671516995 residues
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Medicago sativa
Sukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliopbyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
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ProLysValAlaAspGlyGluAspProTyr11eLysLysLeuValLeuLysGlyLysGln
                                                                                                                                                                  CysLysGluIleIleLeuLysValLeuLysValAsnAspProCysProTyrProSerCys
              TyrAspLeuTyrValHisSerTyrLeuArgPheGlyLysGluAlaThrArgAlaGlnVal
                                                               LeuAsnAlaThrAsnGlySerAlaAsnProCysIleLeuProGlyPheAsnGlyThrPhe
                                                                                                                ThrTyrSerGlyValGluTyrLysAlaPheSerProSerSerGlySerAsnPheAspAsp
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Roberts, N.J., Brigham, J., Wu, B., Murphy, J.B., Volpin, H.,
Phillips, D.A. and Etzler, M.E.
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Roberts, N.J., Brigham, J., Wu, B., Murphy, J.B., Volpin, H. Phillips, D.A. and Etzler, M.E.
A Nod factor-binding lectin is a member of a distinct c apyrases that may be unique to the legumes
Mol. Gen. Genet. 262 (2), 261-267 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AF156782
Medicago sativa nod factor binding lectin-nucleotide phosphohydrolase (LNP) mRNA, complete cds.
AF156782. GI:6006798
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             Navaro-Gochicoa, M.T., Camut, S., Niebel, A. and Cullimore, J.V.
Expression of the Apyrase-Like APY1 Genes in Roots of Medicago truncatula is Induced Rapidly and Transiently by Stress and Not Sinorhizobium mellioti or Nod Factors
Plant Physiol. 131 (3), 1124-1136 (2003)
2 (Dases 1 to 1466)
Cullimore, J.V. and Niebel, A.
                                                                                                                           Direct Submission
Submitted (15-NOV-2002) Laboratoire de Biologie Moleculaire des
Relations Plantes-Microorganismes, INRA-CNRS, Castanet-Tolosan
31326, France
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Conservative:
Mismatches:
Indels:
Gaps:
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LLQQAENVVPIDLHHKTPIRLGATAGLRLLNGDASEKILQAVRDMFSNRSTFNVQPDA
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YVCMDLIYQYVLLVDGFDPLQEITSGKEIEYQDAVLEAAMFLGNAVEAISSLPKFERM
MYFV"
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                                                                                                                                                1 (bases 1 to 1511)
Navarro-Gochicoa,M.T., Camut,S., Niebel,A. and Cullimore,J.V.
Navarro-Gochicoa,M.T., Camut,S., Niebel,A. and Cullimore,J.V.
Expression of the Apyrase-Like APYI Genes in Roots of Medicago
truncatula Is Induced Rapidly and Transiently by Stress and Not by
Sinorhizobium meliloti or Nod Factors
Flant Physiol. 131 (3), 1124-1136 (2003)
                                            Medicago truncatula (barrel medic)
Medicago truncatula
Bukaryota, Viridiplantae; Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids I, Fabales, Fabaceae; Papilionoideae, Trifolieae,
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Cullimore,J.V. and Niebel,A.
Direct Submission
Submitted (15-NOV-2002) Laboratoire de Biologie Moleculaire des
Relations Plantes-Microorganismes, INRA-CNRS, Castanet-Tolosan
31326, France
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Mismatches:
Indels:
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/db_xrefE="GI-2804674"
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Matches:
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/gene="APY1;1"
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VCMDLIYQYVLLVDGFGLDPLQKITSGKEIEYQDAIVEAAWPLGNAVEAISALDRFFER
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                                                                                                                                                              PLN 30-MAR-2001
clone:pKS5-1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (24-MNY-1999) Shunnosuke Abe, University of Ehime, Department of Biological Resources; 3-5-7 Tarumi, Matsuyama, Ehime 70 6856, Japan (E-mail:abe@dpc.ehime-u.ac.jp, URL:http://web-mcb.agr.ehime-u.ac.jp/bunnshi/, Tel:81-899-46-9853, Fax:81-899-46-9853)
               457
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Shibta.K., Morita,Y., Abe,S., Stankovic,B. and Davies,E.
Apyrase from pea stems: Isolation, purification, characterization and identification of a NTPase from the cytoskeleton fraction of
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                             1351 CCTCTAGGCAATGCTGTAGAAGCCATATCATCGTTACCTAAATTTGAACGAATGATGTAT
               ProLeuGlyThrAlaValGluAlaIleSerAlaLeuProLysPheLysArgLeuMetTyr
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Plant Physiol. Biochem. 37, 881-888 (1999)
2 (sites)
2 Shibata,K., Abe,S. and Davies,E.
Structure of the coding region and mRNA variants of gene from pea (Pisum sativum)
Acta Physiol. Plant. (2001) In press
3 (bases 1 to 1648)
Shibata,K. and Abe,S.
Direct Submission
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Pisum sativum mRNA for S-type apyras, complete cds,
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Pisum sativum mRNA for apyrase, complete cds, clone:pKS17-2.
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Submitted (22-FBB-2000) Shunnosuke Abe, Ehime University, College
of Agriculture; Tarumi 3-5-7, Matsuyama, Ehime 790-8566, Japan
(B-mail:abe@mcb.agr.ehime-u.ac.jp,
URL:http://web-mcb.agr.ehime-u.ac.jp, Tel:+81-89-946-9853,
Fax:+81-89-946-9853)
                                                    ileTrpAsnGlyGlyGlyGlySerGlyGlnLysLysLeuPheValThrSerAlaPheAla
                                                                      TyrLeuAlaGluAspValGlyMetValGluProAsnLysProAsnSerIleLeuHisPro
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                                                                                                                                                               ValAspPheGlulleGluAlaLysArgAlaCysAlaLeuAsnPheGluAspValLysSer
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Shibata, K., Abe, S. and Davies, E.
Structure of the coding region and mRNA variants of the apyrase from Pisum Sativum
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148 208 268 104 328 124 388 144 448 164 508 184 568 204 628 88 44 64 224 688 244 748 24 84 32 AIGGAGTICCTIATIAAACTIATC---ACTITICIACIATITICIATGCCTGCAATCACT SerSerGlnTyrLeuGlyAsnAsnLeuLeuThrAsnArgLysIlePheGlnLysGlnGlu MetGluPheLeuIleThrLeuIleAlaThrPheLeuLeuLeuMetProAlaIleThr ThrLeuThrSerTyrAlaValllePheAspAlaGlySerThrGlyThrArgValHisVal 149 GAAATTTCCTCTTACGCTGTCGTATTCGATGCTGGTAGCACTGGTAGTCGCATTCATGTT TyrHisPheAspGlnAsnLeuAspLeuLeuHisIleGlyAsnAspIleGluPheValAsp LyslleLysProGlyLeuSerAlaTyrGlyAspAsnProGluGlnAlaAlaLysSerLeu IleProLeuLeuGluGluAlaGluAspValValProGluAspLeuHisProLysThrPro 125 LeuArgLeuGlyAlaThrAlaGlyLeuArgLeuLeuAsnGlyAspAlaAlaGluLysIle LeuGlnAlaThrArgAsnMetPheSerAsnArgSerThrLeuAsnValGlnArgAspAla ValSerileileAspGlyThrGlnGluGlySerTyrMetTrpValThrValAsnTyrVal LeuGlyAsnLeuGlyLysSerPheThrLysSerValGlyValIleAspLeuGlyGlyGly SerValGlnMetThrTyrAlaValSerLysLysThrAlaLysAsnAlaProLysValAla AspGlyGluAspProTyrlleLysLysLeuValLeuLysGlyLysGlnTyrAspLeuTyr

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                                                                                                                                 Shiraishi,T.
Direct Submission
Submitted (10-SEP-2001) Tomonori Shiraishi, Okayama University;
1-1-1 Tsushima naka, Okayama city, Okayama 700-8530, Japan
(B-mail:tomoshir@cc.okayama-u.ac.jp, Tel:81-86-251-8311,
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 AsnGlySerAlaAsnProCysIleLeuProGlyPheAsnGlyThrPheThrTyrSerGly
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Shiraishi,T.
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/cultivar="midoriusui"
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                                                                                    TOMONORI SHIRAISHI,IWAO FURUSAWA
C12NN15/09,A01H5/00.C07K14/415,C12N9/16,C12N15/00
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Mismatches:
Indels:
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Matches:
    RENGOKAI, ASAHI TECHNO GLASS CORPOS Pisum sativum L. (Garden Pea) PD 2001017176-A/1
PD 23-JAN-2001
PF 02-JUL-1999 JP 1999189129
PR TOMONORI SHIRAISHI, IWAO FURUSA PC C12N15/09, A01H5/00, C07K14/415, FH Key 1. 1368
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                   Pisum sativum L. .(Garden Pea)
JP 2001017176-A/1
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Disease resistant polypeptide, disease resistant gene, method for imparting disease resistance to plant, disease resistance-imparted transformed plant, and nucleotide triphosphate hydrolase.
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Shiraishi, T. and Furusawa, I.
Shiraishi, T. and Furusawa, I.
Shisase resistant polypeptide, disease resistant gene, method for imparting disease resistance to plant, disease resistance-imparted tranformed plant, and nucleotide triphosphate hydrolase Patent: JP 200101716-A 1 23-JAN-2001;
PRESIDENT OF KYOTO UNIVERSITY NIHON NINJIN HAMBAI KYODOKUMIAI
                         SerValGlnMetThrTyrAlaValSerLysLysThrAlaLysAsnAlaProLysValAla
                                           AspGlyGluAspProTyrIleLysLysLeuValLeuLysGlyLysGlnTyrAspLeuTyr
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TTGGGAAATTTAGGGAAAAAGTACACAAAAACAGTTGGAGTAATAGATCTTGGAGGTGGA
                                                                                           ValHisSerTyrLeuArgPheGlyLysGluAlaThrArgAlaGlnValLeuAsnAlaThr
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Acta Physicol. Plant.

(bases 1 to 1812).

Shibata,K. and Abe,S.
Shibata,K. and Abe,S.
Shibata,M. and Abe,S.
Shibata,M. and Abe,S.
Shibata,K. and Abe,S.
Shibata,K. and Abe,S.
Shibata,K. and Abe,S.
Shibata,M. and Abe,S.
Department of Biological Resources; 3-5-7 Tarumi, Matsuyama, Ehime URL:http://web-mcb.agr.ehime-u.ac.jp,
Fax:81-899-46-9853).
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                                                                                                                                                                                                                                                                                                                                                       ATTTGGAATGGTGGAGGAAATGGACAGAAAACCTTTTTGGTTCTTCATCTTTT 1017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACTTATCCATTCTT---CATAAGAAAATGTAGCTTCATATGTATGCATGGATCTTATA 1194
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TATCAGTATGTGTTACTCGTTGATGGATTTGGTCTTGATCCATTGCAAAAGATTACATCA 1254
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Vicieae;
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                                                                                                                                                                                                                        agaagatttaaagecaactgcttacactrcregigecaaactriraataaaageaaaaacaca
                                                                                                                                                                                                                                                       IleLeuLysValLeuLysValAsnAspProCysProTyrProSerCysThrPheGlyGly
 GATGGAGATGATCCATACATCAAGAAGGTTGTACTCAAGGGAATACCATATGATCTTTAT
                                                      ValHisSerTyrLeuArgPheGlyLysGluAlaThrArgAlaGlnValLeuAsnAlaThr
                                                                       ValGluAlaileSerAlaLeuProLysPheLysArgLeuMetTyrPheile 459
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Shibata,K., Abe,S. and Davies,E.
Structure of the coding region and mRNA variants of
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/brotein_id="BAA75506.1"

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VCMDLIXQYVLLVDGFGLDPLQKITSGKEIEYQDAIVEAAMPLGNAVEAISALFKFER
                                                                               Direct Submission
Submitted (12-JAN-1999) Shunnosuke Abe, University of Ehime,
Department of Biological Resources; 3-5-7 Tarumi, Matsuyama, Ehime
790-8566, Japan (E-mail:abe@dpc.ehime-u.ac.jp,
URL:http://web-mcb.agr.ehime-u.ac.jp/bunnshi/, Tel:81-899-46-9853,
Fax:81-899-46-9853)
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 Structure of the coding region and mRNA variants of the apyrase from Pisum Sativum
Acta Physiol. Plant. 20, 3-13 (2001)
2 (bases 1 to 1645).
Shibata, A. and Abe, S.
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338
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62
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Mismatches:
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                                                                                                                                                                                                            organism="Pisum sativum"
                                                                                                                                                                                                                                                        /db_xref="taxon:3888"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (1-1645)
                                                                                                                                                                            Location/Qualifiers
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rosids, eurosids I, Fabales, Fabaceae, Papilionoideae, Vicieae,
GTTTCTATAATTGATGGAACCCAAGAAGGTTCTTATCTATGGGTGACAGTTAACTATGCA
                           LeuGlyAsnLeuGlyLysSerPheThrLysSerValGlyValIleAspLeuGlyGlyGly
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                                                                                                                                                     AspGlyGluAspProTyrileLysLysLeuValLeuLysGlyLysGlnTyrAspLeuTyr
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870 GAAGAGITTAAGGCAACIGCTTACACITCTGGIGCAAACTTTAATAAATGCAAAAACACA
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Pisum sativum mRNA for apyrase, complete cds.
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rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Vicieae;
                                                                                                                                                                                                                                                                                   Shibata,K., Abe,S. and Davies,E.
Structure of the coding region and mRNA variants of the apyrase from Pisum Sativum
Acta Physiol. Plant. 20, 3-13 (2001)
2 (bases 1 to 1648)
Shibate,K. and Abe,S.
Direct Submission
Submitted (22-FBB-2000) Shunnosuke Abe, Ehime University, College Agriculture; Tarumi 3-5-7, Matsuyama, Ehime 790-8566, Japan (B-mall:abe@mcb-agr.ehime-u.ac.jp, Tel:+81-89-946-9853, Fax:+81-89-946-9853,
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Mismatches:
Indels:
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Matches:
                                   Pisum sativum mRNA for apyrase,
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              AB038669
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                LeuArgLeuGlyAlaThrAlaGlyLeuArgLeuLeuAsnGlyAspAlaAlaGluLysIle 144
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SerSerGlnTyrLeuGlyAsnAsnLeuLeuThrAsnArgly8IlePheGlnLy8GlnGlu 44 ThrLeuThrSerTyrAlaValllePheAspAlaGlySerThrGlyThrArgValHisVal 64 85 Arddadcrectrarraaacrrarc---acrrrrcracrarrrerardectaaarcac MetGluPheLeuIleThrLeuIleAlaThrPheLeuLeuLeuMetProAlaIleThr 45 8

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AVPDAGGTSRIHVYHFNQNLDLLHGGYGRYKKITPGESARANDEDARGLIFL
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SILDGTQEGSYLWYTVNYALGNLGRKYYTKTVGVIDLGGGSVQMAYAVSKKTARARAPKA
                                                                                                                                                                                                                                                                            Pisum sativum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Pabales; Pabaceae; Papilionoideae; Vicieae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cloning of the CDNA and expression of the mRNA for a gene encoding a calmodulin-regulated nucleoside triphosphatase associated with the envelope of pea nuclei
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YSGEBFKATAYTSGANFNKCKNTIRKALKLNYPCPYQNCTFGGIWNGGGGNGQRNLFA
SSSFPYLPEDTGMVDASTPNFILRPVDIETKAKEACALNFEDAKSTYPFLDKKNVASY
VCMDLIYQYVLLVDGFGLDPLQKITSGKEIEYQDAIVEAAWPLGNAVBAISALPKFER
                       GlyGluGlyIleGlnTyrGlnAsnSerValValGluAlaAlaTrpProLeuGlyThrAla
                                         Submitted (21-APR-1994) Hsieh H., University of Texas at Austin, Botany, Biological Lab. Rm 6, Austin, Texas, USA, 78713
                                                                                                                                                                                   bp mRNA linear PLN 04-JU
WA for nucleoside triphosphatase.
                                                                                                                                                                                                                                                                                                                                                                                                               in pea
                                                                                    ValGluAlaIleSerAlaLeuProLysPheLysArgLeuMetTyrPheIle
                                                                                                      transport
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Hsieh,H.L., Tong,C.G., Thomas,C. and Roux,S.J.
Light-modulated abundance of an mRNA encoding a
calmodulin-regulated, chromatin-associated NTPase
Plant Mol. Biol. 30 (1), 135-147 (1996)
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/codon_start=1
/product="nucleoside_triphosphatase"
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/function="might be involved
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/clone="p480.1-9"
/tissue_type="plumule"
/clone_lib="pea_plumule cf
/dev_stage="Seedling"
1. 1661
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/strain="Alaska"
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NTPase, nucleoside
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  305 ileLeuLysValLeuLysValAsnAspProCysProTyrProSerCysThrPheGlyGly
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Oy 345 TyrLeuAlaGluAspValGlyMetValGluProAsnLysProAsnSerIleLeuHisPro 364	Db 1296 GGGAAGGAATTGAATACAAGTGCTATTGTGGAAGCTGCATGGCCTTAGGCAATGCT 1355 Qy 443 ValGluhlanleSerAlaLeuProLysPheLysArgLeuMetTyrPheile 459 Db 1356 GTAGAAGCATATCAGCTTTACCTAAATTTGAGCGATTGATGTTTTGTT 1406 RESULT 14 E51055 LOCUS E51055 DEFINITION Disease resistant polypeptide, disease resistant gene, method for	ACCESSION Transformed plant, and nucleotide triphosphate hydrolase. VERNORD E51055. G1:18629461 VERYWRDS TP 2001017176-A/2. SOURCE unidentified Uncleotide triphosphate hydrolase. VERYWRDS UP 2001017176-A/2. SOURCE unidentified Uncleotified Uncleotified NATHORS Shiraishi,T. and Furusawa,I. TITLE Disease resistant polypoptide, disease resistant gene, method for imparting disease resistant polypoptide.	JOURNAL Patent, and nucleotide triphosphate hydrolase patent: JP 201011775-A, 2 23-AN-2001, RESIDENT OF KYOTO UNIVERSITY COMMENT OS Pisum sativum L. (Garden Pea) PN JP 201017176-A/2 PP 20-JAN-2001 PF 02-JUL-1999 JP 1999189129 PR TOMONORI SHIRAISHI, IWAO FURUSAWA PC C12N15/09,A01H5/00,C07K14/415,C12N9/16,C12N15/00 CC FT SOUTCE	FT /or Location/Qualif 11697 /organism="unid /mol_type="geno /db_xref="taxon	Alignment Scores: Pred. No.: 1.11e-151 Length: 1697 Score: Score: Percent Similarity: 85.56% Conservative: 53 Best Local Similarity: 73.96% Mismatches: 62 Query Match: 74.20% Indels: 4 DB: US-09-657-631-4 (1-459) x E51055 (1-1697) QY 5 MetGluPheLeuIleThrLeuIleAlaThrPheLeuLeuLeuWetProAlaileThr 24
Best Local Similarity: 73.96\$ Mismatches: 62 4 Query Match: 6 74.20\$ Indels: 3 DB: 6 Gaps: 3 5 OS-657-631-4 (1-459) x E51056 (1-1667) OY S MetGluPheLeulleThrLeulleAlaThrPheLeuLeuLeuWetProAlaIleThr 24 OY ATGAGTTCCTTATAAACTTATC - ACTTTCTATCTATCTATCTATCTATCTATCTATCTATCT	219 TACCATTTTAACCAGAACTTAGACCTTCTCATATTGGCAAAGGTGTCGAGTATTATAAT 85 LysIleLysProGlyLeuSerAlaTyrGlyAspAsnProGluGInAlaAlaLysSerLeu 105 LysTleLysProGlyLeuSerAlaTyrGlyAspAsnProGluGInAlaAlaLysSerLeu 279 AAGATAACACCTGGTTTGAGTTCATACGCTAATAATCCAGAACAGGCTGCAAAATCTCTC 105 IleProLeuLeuGluGluAlaGluAspValValProGluAspLeuHisProLysThrPro 110 IleProLeuLeuGluGluAlaGluAsgValValProGluAspLeuHisProLysThrPro 111	OY 125 LeuArgLeuGlyAlaThrAlaGlyLeuArgLeuLeuAsnGlyAspAlaAlaGluLysile 144 139 GTTAGACTTGGGGCAACTGCCGGTTTAGATGGATGCTTTGAAAGATA 458 OY 145 LeuGlaAlaThrArgAsnWetPheSerAsnArgSerThrLeuAsnValGlnArgAspAla 164	Qy 185 LeuGlyAsnLeuGlyLysSerPheThrLysSerValGlyVallleAspLeuGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyG	Oy 245 ValHisSerTyrLeuArgPheGlyLysGluAlaThrArgAlaGlnValLeuAsnAlaThr 264	Cy 285 ValGluTyrLyshlaPheSerProSerSerGlySerAsnPheAspaspCysLysGluIle 304 1

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                                                                                                                                                                                                                                                                                       mRNA, complete
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                                                                                   TyrdlnHisValLeuLeuValHisGlyPheGlyLeuGlyProArgLysGlulleThrVal
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                                                                                                       LysileLysProGlyLeuSerAlaTyrGlyAspAsnProGluGlnAlaAlaLysSerLeu
                           SerSerGlnTyrLeuGlyAsnAsnLeuLeuThrAsnArgiysIlePheGlnLysGlnGlu
                                                                                                                                               TyrHisPheAspGlnAsnLeuAspLeuLeuHisIleGlyAsnAspIleGluPheValAsp
ATGGAGTTCCTTATTAAACTTATC---ACTTTTCTACTATTTTCTATGCCTGCAATCACT
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Aac39492 Ada70915

Rice gene Rice gene NBP46 (ro

Rice gene DNA clone Rice gene Arabidops

DNA clone Drosophil Drosophil

Ada96075 Ada69716 Ada70175 Ada70759 Ada7029 Ada70240 Ada70240 Ada70240 Ada70289 Ada70289 Ada70289 Ada70289 Ada7029 Ada

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Aaz50357 Aaf63385 Aaf63418 Aaa96066

Arabidops Arabidops Arabidops

Abz42130 Ada68447 AAbz13044 Ada68468 A

Arabidops

Run on:

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NBP46; lectin; Rhizobium; leguminous plant; transgenic plant; nitrogen; nitrogen fixation; fertilizer; ss.
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ABZ14083
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ADA68447
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AAC39492
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ADA70759
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REGC ) UNIV CALIFORNIA.
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Medicago sativa.
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-MODEL=frame+_p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO spool/US09657631/runat_10082004_171045_1662/app_query.fasta_1.1294
-Q=/cgn2_1/USPTO spool/US09657631/runat_10082004_171045_1662/app_query.fasta_1.1294
-Q=-Read_2957m04 -QFMT=fastap -SUFFIX=p2n.rng -MNNATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -GTART=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL_OUTFNT=ptc -NOFM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USDE=LOCAL_OUTFNT=ptc -NOFM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USDE=LOCAL_OUTFNT=ptc -NOFM=0 - THR_T -DSPENOCK=100 -LONGLOG
-DOWNADP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPENOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FCAPPOP=6
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Aaf85679 Pea bligh
Aaa96064 Ecto-phos
Aaf85681 Pea bligh
Aak85680 Pea bligh
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Aax08522 NBP46 (ro
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Copyright (c) 1993 - 2004 Compugen Ltd.
                                        nucleic search, using frame_plus_p2n model
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ThrPheGlyGlyIleTrpAsnGlyGlyGlyGerGlyGlnLysLysLysLeuPheValThr 340
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                                                                                CCTAAAGTIGCIGAIGGAGAGAICCAIAIAITAAAAACTIGIGCICAAGGGAAAGCAA
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LeuGlyGlyGlySerValGlnMetThrTyrAlaValSerLysLysThrAlaLysAsnAla
                 ProLysValAlaAspGlyGluAspProTyrIleLysLysLeuValLeuLysGlyLysGln
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Modulating mycorhizal infection, useful for improving plant growth, transforming plant cell with a sequence encoding lectin/nucleotide phosphohydrolase.
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transl except (pos.1378. .1380, aa.Xaa)
transl except (pos.1378. .1380, aa.Xaa)
transl except (pos.1408. .1410, aa.Xaa)
// transl except (pos.1435. .1437, aa.Xaa)
// note "Xaa Stop codon"
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                                    GluPheValAspLysIleLysProGlyLeuSerAlaTyrGlyAspAsnProGluGlnAla
                                                            241 GAGTITGTTGACAAGAICAAACCAGGTITGAGTGCATAIGGGGAIAATCCTGAACAAGCA
                                                                                                                                       GlnArgAspAlaValSerIleIleAspGlyThrGlnGluGlySerTyrMetTrpValThr
                                                                                                                 AlaLysSerLeuIleProLeuGluGluAlaGluAspValValProGluAspLeuHis
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                  11eProLeuLeuGluGluAlaGluAspValValProGluAspLeuHisProLysThrPro
                                                                  298 ATTCCACTTTTAGAGCAAGCAGAAGATGTCGTCCCCGAGGATCTTCAACCCAAGACACCC
                                                                                             LeuArgLeuGlyAlaThrAlaGlyLeuArgLeuLeuAsnGlyAspAlaAlaGluLysIle
                                                                                                                                                                       ValSerIleIleAspGlyThrGlnGluGlySerTyrMetTrpValThrValAsnTyrVal
                                                                                                                                                                                   TACCATTTTAACCAGAACTTAGACCTTCTTCATATTGGCAAAGGTGTCGAGTATTATAAT
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              459
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                                                                                                                                                                                                                                                                                                                                                                New blight-resistant polypeptide useful for giving blight resistance
             ds
                                                                                                                                                  Pea; blight resistance; nucleotide triphosphate decomposition;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               BP; 422 A; 260 C; 275 G; 411 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1368
338
53
62
4
                                                                                                                                                                                                                     "blight resistance protein"
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                               resistance protein coding sequence #1
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                                                                                                                                                                                       Location/Qualifiers
1. .1368
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1769.00
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73.96%
                                                                        DNA; 1368
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                                                                        AAF85679 standard;
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Best Local Similarity:
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                                                                                                                                                                      Pisum sativum
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1182 ACTTATCCATTTCTT---GATAAGAAAATGTAGCTTCATATGTATGCATGGATCTTATA 1238
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                                          LysileLysProGlyLeuSerAlaTyrGlyAspAsnProGluGlnAlaAlaLysSerLeu
                                                                                             402 GTTAGACTTGGGGCAACTGCCGGTTTAAGGCTTTTGAATGGAGATGCTTCTGAAAAGATA
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                                                                                                                                    IleProLeuLeuGluGluAlaGluAspValValProGluAspLeuHisProLysThrPro
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                         TyrHisPheAspGlnAsnLeuAspLeuLeuHisIleGlyAsnAspIleGluPheValAsp
                                                                                                                                                             342 ATTCCACTITIAGAGCAAGCAGAAGATGTCGTCCCCGACGATCTTCAACCCAAGACACCC
                                                                                                                                                                                                                                                             SerValGlnMetThrTyrAlaValSerLysLysThrAlaLysAsnAlaProLysValAla
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             265 AsnGlySerAlaAsnProCysIleLeuProGlyPheAsnGlyThrPheThrTyrSerGly
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to a method for increasing or decreasing drug resistance in target bacteria, yeast, plant or mammalian cells by altering the ATP gradient across the biological membrane of the target cell. The method is useful for modulating drug resistance of cells. It is useful for increasing the sensitivity of cells to chemcheraputic and antibiotic agents and increasing resistance to herbicides. The present sequence is from Pisum sadivum and encodes an ecto-phosphatase (extracellular phosphatase). This sequence was used in the present invention to modulate drug resistance. Note: The present sequence is not shown in the specification, but is referred to via its GenBank accession number
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Increasing or decreasing drug resistance in target bacteria, yeast, plant or mammalian cells comprises altering ATP gradient across biological membrane of target cell.
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     chemotheraputic;
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338
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                                                                                                                                                                                                 resistance, ATP gradient; chextra-cellular phosphatase;
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                        SJ,
                                                                                                                                                                     Ecto-phosphatase coding sequence
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1769.00
85.56%
73.96%
74.20%
                                                                                      AAA96064 standard; DNA; 1661
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                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                       Windsor JB,
                                                                                                                                                                                              Ecto-phosphatase; drug antibiotic; herbicide;
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                                                                                                                                                                                                                                                                                                                                                                             (TEXA ) UNIV TEXAS
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Best Local Similarity:
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                                                                                                                                                                                                                   ValSerileIleAspGlyThrGlnGluGlySerTyrWetTrpValThrValAsnTyrVal
                                                                                                                                                                                                                               SerValGlnMetThrTyrAlaValSerLysLysThrAlaLysAsnAlaProLysValAla
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.59 GAAATTTCCTCTTACGCTGTCGTATTCGATGCTGGTAGCACTGGTAGTCGCATTCATGTT
                               LysileLysProGlyLeuSerAlaTyrGlyAspAsnProGluGlnAlaAlaLysSerLeu
                                                                                                 IleProLeuLeuGluGluAlaGluAspValValProGluAspLeuHisProLysThrPro
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                    TyrHisPheAspGlnAsnLeuAspLeuLeuHisIleGlyAsnAspIleGluPheValAsp
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                          The present invention provides the protein and coding seguences of a pea
protein with nucleotide triphosphate decomposing activity. The gene can
be used for conferring blight resistance on a plant. The present sequence
is one version of the coding sequence of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                              polypeptide useful for giving blight resistance
                                                                                                                                                                                           ds.
                                                    Pea; blight resistance; nucleotide triphosphate decomposition;
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/product= "blight resistance protein"
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 5; Page 13-14; 20pp; Japanese.
                                                                                                                                                                                                                                Location/Qualifiers
42. .1409
/*tag= a
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P-PSDB; AAB81952.
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Best Local Similarity:
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Pred. No.:
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                                                                                  LysIleLysProGlyLeuSerAlaTyrGlyAspAsnProGluGlnAlaAlaLysSerLeu 104
                                                                                                    262 AAGATAACACCTGGTTTGAGTTCATACGCTAATAATCCAGAACAGGCTGCAAAATCTCTC 321
                                                                                                                                                                                                                                                             LeuGlnalaThrArgAsnMetPheSerAsnArgSerThrLeuAsnValGlnArgAspAla 164
142 GAAATTTCCTCTTACGCTGTAGTATTCGATGCCGGTAGCACTGGTAGTCGCATTCATGTT 201
                                                                                                                                                                                                                         ValGluTyrLysAlaPheSerProSerSerGlySerAsnPheAspAspCysLysGluIle 304
                         TyrHisPheAspGlnAsnLeuAspLeuLeuHisIleGlyAsnAspIleGluPheValAsp
                                                                                                                                                               ValSerIleIleAspGlyThrGlnGluGlySerTyrMetTrpValThrValAsnTyrVal
                                                                                                                                           105 IleProLeuLeuGluGluAlaGluAspValValProGluAspLeuHisProLysThrPro
                                                                                                                                                                                                   LeuArgLeuGlyAlaThrAlaGlyLeuArgLeuLeuAsnGlyAspAlaAlaGluLysIle
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                                                                                                                                                                                                                                                                                LeuGlyAsnLeuGlyLysSerPheThrLysSerValGlyVallleAspLeuGlyGlyGly
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     305 IleLeuLysValLeuLysValAsnAspProCysProTyrProSerCysThrPheGlyGly
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  365 ValAspPheGluIleGluAlaLysArgAlaCysAlaLeuAsnPheGluAspValLysSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         265 AsnGlySerAlaAsnProCysIleLeuProGlyPheAsnGlyThrPheThrTyrSerGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Grcdatarrdagacraaagcraaagaagcrrdcgcgrrraaacrrcgaggargcgaaarcr
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                                       1355
            442
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SerSerGlnTyrLeuGlyAsnAsnLeuLeuThrAsnArgLysIlePheGlnLysGlnGlu 44
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    GlyGluGlyIleGlnTyrGlnAsnSerValValGluAlaAlaTrpProLeuGlyThrAla
                        ThrLeuThrSerTyrAlaValllePheAspAlaGlySerThrGlyThrArgValHisVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      {\tt MetGluPheLeuIleThrLeuIleAlaThrPheLeuLeuLeuLeuMetProAlaIleThr}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New blight-resistant polypeptide useful for giving blight resistance
                                                                                                                                                                                                                                                                   Pea; blight resistance; nucleotide triphosphate decomposition; ds.
                                                                                    GTAGAAGCCATATCAGCTTTACCTAAATTTGAGCGATTGATGTATTTTGTT 1406
                                                              ValGluAlaileSerAlaLeuProLysPheLysArgLeuMetTyrPhelle 459
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                                                                                                                                                                                                                                            sequence #2
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Matches:
Conservative:
Mismatches:
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Gaps:
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                                                                                                                                                                                                                                        Pea blight resistance protein coding
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25. 1392
/*tag= a
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                                                                                                                                                    AAF85680 standard; DNA; 1697 BP
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Best Local Similarity:
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Mismatches:
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   Sequence 1489
                                         Scores:
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                           GlyGluGlyIleGlnTyrGlnAsnSerValValGluAlaAlaTrpProLeuGlyThrAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Modulating mycorhizal infection, useful for improving plant growth, transforming plant cell with a sequence encoding lectin/nucleotide phosphohydrolase.
                                                                                                                   1339 GTAGAAGCCATATCAGCTTTACCTAAATTTGAGCGATTGATGTATTTGTT 1389
                                                                                                                                                                                                                                                                                                         DNA encoding Medicago sativa lectin/nucleotide phosphohydrolase,
                                                                                                                                                                                                                                                                                                                                          Lectin/nucleotide phosphohyrdolase; LNP; mycorrhizal infection; carbohydrate binding protein; nucleotide dephosphorylation; oligosaccharide signalling; nutrient uptake; plant growth; plant development; antisense technology; gene; ds.
                                                                                ValGluAlaIleSerAlaLeuProLysPheLysArgLeuMetTyrPheIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product= "LNP"
/note= "Lectin/nucleotide phosphohydrolase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /hote= "No start or stop codon given"
/ransl_except= (pos:22. .24, aa:Xaa)
/ransl_except= (pos:1411. .1413, aa:Xaa)
/ransl_except= (pos:1453. .1455, aa:Xaa)
/note= "Xaa= Stop codon"
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P-PSDB; AAU78820.
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The production of transgenic plants comprising an expression caseette expressing the NBP46 root lectin is advantageous since it would mean that non-leguminous plants could fix nitrogen from the atmosphere, lessening the need for the addition of nitrogen containing fertilizer to soil This would lead to higher crop yields where soil has been overplanted and replenishment of the depleted soil with usable nitrogen. Alternatively, the plant. The nucleic acid sequences can be used to modulate oligosaccharide signalling in the plant. The nucleic acid sequences can be used to inhibit expression of an endogenous gene and also to suppress endogenous NBP46 gene
                                                                                                                                                                                                                                                                                                                                                                                                          rhizobial bacteria via a lectin-carbohydrate interaction.
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                                                                                                                                                                                                                                                                                                                                                       LysAsnMetGluPheLeuIleThrLeuIleAlaThrPheLeuLeuLeuLeuMetProAla
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                                                                                                                                                                                       1111 AAAATTCGTCCAGTTGATTTGAAGACTGCAGCTAAACTAGCTTGTAAAACAAATCTTGAG
                                                                                                                                                                                                                   381 ASPValLysSerThrTyrProArgLeuThrAspAlaLysArg---ProTyrValCysMet
CysLysGlullelleLeuLysValleuLysValAsnAspProCysProTyrProSerCys
                                                                                                        SerAlaPheAlaTyrLeuAlaGluAspValGlyMetValGluProAsnLysProAsnSer
                                                                                                                       1054 TCATCTTTCTATTACTCTCTGAAGATGTTGGG---ATCTTTGTGAATAAACCCAATGCC
                        934 IGCAGAAAGAIAGCICIIIAAGGCICTIAAAGIGAAIGCACCIIGICCCIAICAGAAIIGC
                                                    ThrPheGlyGlyIleTrpAsnGlyGlyGlyGlySerGlyGlnLysLysLysLeuPheValThr
                                                                        994 ACTITIGGIGGGATAIGGAAIGGIGGAGGIGGAAGIGGICAAAAAAAATCTITICCITACI
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1291 GTTACAGTGGCGAATGAAATTCAAGATGCTCTTGTGGAAGCCGCATGGCCTCTA
                                                                                                                                                                                                                                                                         400 AspleuLeuTyrGlnHisValLeuLeuValHisGlyPheGlyLeuGlyProArgLysGlu
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                                                                    Etzler ME,
14-MAR-2002
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                                                                                                                                                                                                                                       VallysSerThrTyrProArgLeuThrAspAlaLysArgProTyrValCysMetAspLeu 401
                                                                        AlaPheAlaTyrLeuAlaGluAspValGlyMetValGluProAsnLysProAsnSerIle
                                                                                                                                 PheGlyGlyIleTrpAsnGlyGlyGlyGlySerGlyGlnLysLysLeuPheValThrSer
                                                                                                                                                                                                                                                                                                          ValGlyGluGlyIleGlnTyrGlnAsnSerValValGluAlaAlaTrpProLeuGlyThr
GACCTTTATGTTCACAGTTACTTGCGTTATGGTAACGACGCAGCACGTGTTAAAGATTTT
                           AsnAlaThrAsnGlySerAlaAsnProCysIleLeuProGlyPheAsnGlyThrPheThr
                                     TyrserglyvalGluTyrLysAlaPheSerProSerSerGlySerAsnPheAspAspCys
                                                                                               LysGlullelleLeuLysValLeuLysValAsnAspProCysProTyrProSerCysThr
                                                                                                                                                                                                                                                                                                                                                      encoding Dolichos biflorus lectin/nucleotide phosphohydrolase,
                                                                                                                                                                                                                                                                                                                                             AlaValGluAlaileSerAlaLeuProLysPheLysArgLeuMetTyrPheIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lectin/nucleotide phosphohyrdolase; LNP; mycorrhizal infection; carbohydrate binding protein, nucleotide dephosphorylation; oligosaccharide signalling; nutrient uptake; plant growth; plant development; antisense technology; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'note= "Lectin/nucleotide phosphohydrolase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /*tag= a
195. .1436
/*tag= c
/label= Mature_LNP
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                                                                                                                                                                                                                                                                                                                                                                                                 BP.
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The invention describes a method of modulating mycorrhizal infection by introducing into a plant an expression cassette comprising a plant promoter operably linked to a heterologous LNP (lectin/nucleotide phosphorytoclase) polynucleotide, or its complement. The LNP's described in the invention are involved in binding a variety of carbohydrates, catalysing the dephosphorylation of nucleotide di- and tri-phosphates and are suspected to be involved in olingosaccharide signalling, important for the interaction of mycorrhizal fungi and plants. The method is useful to increase mycorrhizal infection (by increasing expression of the polynucleotide), resulting in increased uptake of nutrients by plants and better growth/development, but antisense (or other methods of) suppression of LNP expression is also contemplated. This sequence encodes the Dolichos biflorus lectin/nucleotide phosphohydrioase (LNP) that can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LysSerLeulleProLeuLeuGluGluAlaGluAspValValProGluAspLeuHisPro 121
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                                                                                                                                                                                                                                                                                           Modulating mycorhizal infection, useful for improving plant growth, transforming plant cell with a sequence encoding lectin/nucleotide phosphohydrolase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           347 G; 474 T; 0 U; 0 Other;
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307
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Matches:
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1654.50
82.75%
67.03%
                                                    06-SEP-2000; 2000US-00657631.
2001WO-US028165
                                                                                                         (REGC ) UNIV CALIFORNIA
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248

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368

308 101

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(root lectin) cDNA.
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|1143 AATCGCCCTCTGGATTTTGAAACTGCAGCTAAACATGGAGCTTGTAGTTTAACATTCGAGGAA 1202
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                                                                                                                       GluLysileLeuGlnAlaThrArgAsnMetPheSerAsnArgSerThrLeuAsnValGln
                    489 GAAAAGATATTGCAAGCGGTTAGGGAAATGTTCAGGAACAGAAGTTCCCTGAGCGTTCAA
                                                AsnTyrValLeuGlyAsnLeuGlyLysSerPheThrLysSerValGlyValIleAspLeu
                                                                                  LysValAlaAspGlyGluAspProTyrIleLysLysLeuValLeuLysGlyLysGlnTyr
                                                                                                                                                                                                                    262 AsnAlaThrAsnGlySerAlaAsnProCysIleLeuProGlyPheAsnGlyThrPheThr
                                      162 ArgAspAlaValSerIleIleAspGlyThrGlnGluGlySerTyrMetTrpValThrVal
                                                                                                           GlyGlyGlySerValGlnMetThrTyrAlaValSerLysLysThrAlaLysAsnAlaPro
                                                                                                                                                                                                                                                      TyrSerGlyValGluTyrLysAlaPheSerProSerSerGlySerAsnPheAspAspCys
                                                                                                                                                                                                                                                                     909 TATICCGGAGAAICGIACAAIAICIAIGGICCCACIICIGGIGCCAACIIIAAAIGAGIGC
                                                                                                                                                                                                                                                                                         LysGluIleIleLeuLysValLeuLysValAsnAspProCysProTyrProSerCysThr
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The NBP46 root lectin is instrumental in recognising and binding to nitrogen fixing rhizobial bacteria via a lectin-carbohydrate interaction. The production of transpenic plants comprising an expression cassette expressing the NBP46 root lectin is advantageous since it would mean that non-leguminous plants could fix nitrogen from the atmosphere, lessening the need for the addition of nitrogen containing fertilizer to soil. This would lead to higher crop yields where soil has been overplanted and replenishment of the depleted soil with usable nitrogen. Alternatively, the plant. The nucleic acid sequences can be used to inhibit expression of an endogenous gene and also to suppress endogenous NBP46 gene
NBP46; lectin; Rhizobium; leguminous plant; transgenic plant; nitrogen;
                                                                                                                                                                    /note= "These bases represent nucleotides missing from the sequence given in the specification. They are included to maintain the nucleotide numbering given in
                                                                                                                                                                                                                                                                                                                                                                                                                            from
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                                                                                                                                                                                                                                                                                                                                                                                                               /note= "These bases represent mucleotides missing
the sequence given in the specification. They are
included to maintain the nucleotide numbering give
the specification for this sequence"
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production of transgenic plants which are able to fix nitrogen.
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Conservative:
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Indels:
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                                                                                                                           ocation/Qualifiers
                           nitrogen fixation; fertilizer; ss
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P-PSDB; AAW85686.
                                                                           Lotus japonica
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Gaps:

Percent Similarity: Best Local Similarity:

Query Match: DB:

(first entry)

19-JUL-1999

AAX08529

standard;

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1230

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459

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The NBP46 root lectin is instrumental in recognising and binding to nitrogen fixing rhizobial bacteria via a lectin-carbohydrate interaction. The production of transgenic plants comprising an expression cassette expressing the NBP46 root lectin is advantageous since it would mean that non-leguminous plants could fix nitrogen from the atmosphere, lessening the need for the addition of nitrogen containing fertilizer to soil. This would lead to higher crop yields where soil has been overplanted and replenishment of the depleted soil with usable nitrogen. Alternatively,
                                                                                                                                                                                                                             NBP46; lectin; Rhizobium; leguminous plant; transgenic plant; nitrogen;
                                                                            400 AspleuLeuTyrGlnHisValLeuLeuValHisGlyPheGlyLeuGlyProArgLysGlu
                                                                                                                                  1231 GAİCİİGETCIACGEGERACALTIĞCİTĞİTİĞATĞGAİTİTĞĞIÇİTĞBETÇÇALTICAAĞAĞ
                                                                                                                                                                                                                GlyThrAlaValGluAlaIleSerAlaLeuProLysPheLysArgLeuMetTyrPheIle
  361 IleLeuHisProValAspPheGluIleGluAlaLysArgAlaCysAlaLeuAsnPheGlu
                           1111 AAAATTCGTCCAGTTGATTTGAAGACTGCAGCTAAACTAGCTTGTAAAACAAATCTTGAG
                                                     AspvallysserThrTyrProArgleuThrAspAlaLysArg---ProTyrValCysMet
                                                                                                                                                             11eThrvalGlyGluGlyIleGlnTyrGlnAsnSerValValGluAlaAlaTrpProLeu
                                                                                                                                                                            New polynucleotides encoding Nod factor binding lectins - useful production of transgenic plants which are able to fix nitrogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           polypeptide"
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1. .1404
/*tag= a
/product= "DBX polype
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                                                                                                                                                     154 AAAAATCAGGAACCAGTTACATCATACGCTGTTATATTTGATGCTGGTAGCACTGGAAGC
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expression of NBP46 can be used to modulate oligosaccharide signalling in the plant. The nucleic acid sequences can be used to inhibit expression of an endogenous gene and also to suppress endogenous NBP46 gene expression. This DBX sequence also isolated from D. biflorus is also involved in oligosaccharide signalling
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                                                                                                                                                                                                                             SerSerGlnTyrLeuGlyAsnAsnLeuLeuThrAsnArgLysIle---
                                                                                                                                                                                                                                                                                    64 ACTGCAACTGCAAGTTCCTTTTCCCTCCATGGGAAGGGCTTCAAGCATCGCAAGTTTTCC
                                                                                                                                                                                                                                                                                                           ------SerTyrAlaValllePhe
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Identifying a stress condition to which a plant cell has been exposed and
            844 TCTGGTTTTGATGGTATTACACATACGGAGGTCCAGTATAAAGCCACAGCTCCCCT
                                         SerGlySerAsnPheAspAspCysLysGluIleIleLeuLysValLenLysValAsnAsp
                                                         354 GluProAsnLysProAsnSerIleLeuHisProValAspPheGluIleGluAlaLysArg
                                                                                                                                                                                                                     374 AlaCysAlaLeuAsnPheGluAspValLysSerThrTyrProArgLeuThrAspAlaLys
                                                                                                                                                                                                                                       314 ProCysProTyrProSerCysThrPheGlyGlyIJIIITrpAsnGlyGlyGlyGlySerGly
                                                                                                                                                                                                                                                                                                                          GluAlaAlaTrpProLeuGlyThrAlaValGluAlaIleSerAlaLeuProLysPheLys
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                                                                                                                                                                                                                                                                  394 ArgProTyrValCysMetAspLeuLeuTyrGlnHisValLeuLeuValHisGlyPheGly
                                                                                                                                                                                                                                                                                                           414 LeuGlyProArgLysGluIleThrValGlyGluGlyIleGlnTyrGlnAsnSerValVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana stress regulated gene SEQ ID NO 1888
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26-JAN-2001; 2001US-0264647P.
22-JUN-2001; 2001US-0300111P.
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                                                                       GlyGlyGlyGlySerGlyGlnLysLysLeuPheValThrSerAlaPheAlaTyrLeuAla
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                                                                                                               AsnProCys11eLeuProGlyPheAsnGlyThrPheThrTyrSerGlyValGluTyrLys
                                                                                                                                                                                            TyrGlnAsnSerValValGluAlaAlaTrpProLeuGlyThrAlaValGluAlaIleSer
ProTyrileLysLysLeuValLeuLysGlyLysGlnTyrAspLeuTyrValHisSerTyr
                     TCATATGTCAGAGAGATGTATCTGAAGGGACGGAAGTATTTCCTCTATGTTCACAGTTAC
                                                                                                                                                                        AlaPheSerProSerSerGlySerAsnPheAspAspCysLysGluIleIleLeuLysVal
                                                                                                                                                                                                                           LeuLysValAsnAspPro---CysProTyrProSerCysThrPheGlyGlyIleTrpAsn
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                                                                         the invention reactes to interioring a circumstance of the plant cell has been exposed, comprising: (a) contacting nucleic acid from representative of expressed polynucleotides in the plant cell with an array or probes representative of the plant cell genome; and (b) detecting a profile of expressed polynucleotides in the plant cell characteristic of a stress response. The method is useful in the plant cell production of transgenic plants, cells and seeds and in producing plants with increased tolerance to abject stress. The present sequence is that of an Arabidopsis thaliana stress regulated gene (ABZ12196-ABZ17574) used in methods of the invention. Note: The sequence data for this patent is not represented in the printed specification but is based on sequence information supplied to Derwent by the European Patent Office
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                                                              invention relates to identifying a stress condition to which a plant
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    plants with increased tolerance to these abiotic stresses
                                   SEQ ID NO 1888; 577pp + Sequence Listing; English
                                                                                                                                                                                                                                                      Sequence 1419 BP; 377 A; 277 C; 380 G; 385 T; 0 U; 0 Other;
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The invention relates to a novel isolated polynucleic acid segment modulated within a cell by posttranscriptional gene silencing (PTGS). The invention specifically relates to a method to identify an expression product that is modulated by PTGS. The polynucleotide is useful for polynucleic acid into a cell and expressing the nucleic acid segment in the cell to form a product. The polynucleic acid segment is also useful for augmenting a cell and expressing the nucleic acid segment in for augmenting a plant cell with the segment to produce a transformed plant cell, and growing the transformed plant cell, to produce a differentiated transformed plant cell, and MEZ42017 - MEZ42142 represent segments of A. thaliana cDNA modulated by PTGS
                                                                                                                                                                                   Novel polynucleic acid segment useful for modulating within a cell by posttranscriptional gene silencing, plant cell genome.
                                                                                             Wang X,
                                                                                                                                                                                                                                                             Claim 18; Page 411; 438pp; English.
                                      SYNGENTA PARTICIPATIONS
                                                      FRIEDRICH MIESCHER INST
06-APR-2001; 2001US-0282049P.
                                                                                           Meins F,
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P-PSDB; ABP81286.
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91 Ariencircarcercerrcirciecraneceregeagaresarriciearrecere 150 AlaThrAlaGlyLeuArgLeuLeuAsnGlyAspAlaAlaGluLysIleLeuGlnAlaThr 148 |||| ::: ||||||| ||| || || || || || ||| ||| ||| ||| ||| ||| || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || 9 IleThrieuIleAlaThrPheLeuLeuLeuLeuMetProAlaIleThrSerSerGlnTyr GlnAsnLeuAspLeuLeuHisIleGlyAsnAspIleGluPheValAspLysIleLysPro GlyLeuSerAlaTyrGlyAspAsnProGluGlnAlaAlaLysSerLeuIleProLeuLeu GluGluAlaGluAspValValProGluAspLeuHisProLysThrProLeuArgLeuGly ArgAsnMetPheSerAsnArgSerThrLeuAsnValGlnArgAspAlaValSerIleIle 29 LeuGlyAsnAsnLeuLeuThrAsnArgLysllePheGlnLysGlnGluThrLeuThrSer TyrAlavalilePheAspAlaGlySerThrGlyThrArgValHisValTyrHisPheAsp GGGTTGAGGGGCATATCCTACTGATCCCCGACAAGCAGCAAACTCTTTGGTGTCTCTTCTT Conservative: Mismatches: Indels: Length: Matches: (1-1419)US-09-657-631-4 (1-459) x ABZ42130 26e-112 1202.50 71.20% 51.02% 50.44% Percent Similarity: Best Local Similarity: Alignment Scores: 151 49 129 149 69 83 109 331 391 Query Match: Pred. No.: ð ð g g à à P ð qq ò ద à g ò

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                                            GlyLysSerPheThrLysSerValGlyValIleAspLeuGlyGlyGlyGlySerValGlnMet 208
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                                                                                                        TCATATGTCAGAGAGATGTATCTGAAGGGACGGAAGTATTTCCTCTATGTTCACGGTAC
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                                                                                                                                     ProTyrIleLysLysLeuValLeuLysGlyLysGlnTyrAspLeuTyrValHisSerTyr
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The present invention relates to a method (M1) for identifying genes involved in plant resistance or response to pathogenic infection. MI comprises identifying a gene whose expression is significantly altered in the incompatible interaction of plant gene expression relative to expression of the gene in an uninfected plant, in a mutant plant that does not express a gene associated with response to pathogenic infection, or in a corresponding incompatible or compatible interaction. (M1) is useful for conferring resistance to resistance or tolerance to a plant to bacterial, fungal or yiral infection. The present sequence was used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCTACTGCAGGTTTGAGGACGCTGGGTCATGATGCATCTGAGAACATTTTGCAAGCGGTT 510
                                                                                                                                                                                                                     Identifying at least one gene involved in plant resistance or response pathogenic infection for conferring resistance or tolerance to a plant bacterial, fungal or viral infection by determining or detecting plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AlaThrAlaGlyLeuArgLeuAsnGlyAspAlaAlaGluLysIleLeuGlnAlaThr
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GTTGAAGAGTATTCTGTGCATAATCGCAAAGGAGGTCCTAATTCGAGAGGAGGAGAT
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          GlyLysSerPheThrLysSerValGlyValIleAspLeuGlyGlySerValGlnMet
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The invention relates to identifying a stress condition to which a plant cell has been exposed, comprising: (a) contacting nucleic acid representative of expressed polymucleotides in the plant cell with an array or probes representative of the plant cell genome, and (b) detecting a profile of expressed polymucleotides in the plant cell characteristic of a stress response. The method is useful in the production of transgenic plants, cells and seeds and in producing plants with increased tolerance to abiotic stress. The present sequence is that of an Arabidopsis thaliana stress regulated gene (ABZ12196-ABZ17574) used in methods of the invention. Note: The sequence data for this patent is not represented in the printed specification but is based on sequence
                                                                                                                                                                                                                                                                                                                                                                                                                        Identifying a stress condition to which a plant cell has been exposed and producing plants with increased tolerance to these abiotic stresses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     information supplied to Derwent by the Buropean Patent Office
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 144; SEQ ID NO 849; 577pp + Sequence Listing; English.
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                                    thaliana; plant; gene; stress; transgenic; ds
Arabidopsis thaliana stress regulated gene SEQ ID NO
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(SYGN ) SYNGENTA PARTICIPATIONS AG.
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26-JAN-2001; 2001US-0264647P.
22-JUN-2001; 2001US-0300111P.
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                                                                        Arabidopsis thaliana
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Copyright (c) 1993 - 2004 Compugen Ltd.
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August 19, 2004, 14:05:21; Search time 3544.42 Seconds (without alignments) 3867.136 Million cell updates/sec 2384 1 QIKUMEFLITLIATFLLLLM......GTAVEAISALFKFKRLMYFI 459 - nucleic search, using frame_plus_p2n model US-09-657-631-4 Title: Perfect score: OM protein Sequence: Run on:

Xgapop 10.0 , Xgapext Ygapop 10.0 , Ygapext Fgapop 6.0 , Fgapext Delop 6.0 , Delext **BLOSUM62** Scoring table:

55026578 27513289 seqs, 14931090276 residues of hits satisfying chosen parameters: Total number Searched:

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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database

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7	879	٠,	u,	12	5310	53104 NF038F11
	869	36.5	652	12	038	NF010D11
υ,	863	٠,	ഗ	10	3459	34590 N210666e
D T C	854	'n,		13	1841	18414 NF068A12
77	ມຸ	'n.	N 1	77	7292	72922 NF091F05
77.	2.248		ωι	77	5000	5005 NF004G10
£1;	842	ω, i	יוט	12	5573	55733 NF093B10
14	۳,	<u>.</u>	യ	10	2570	25702 NF055F11
15	834.5	'n.	വ	12	5747	57472 NF106A03
16	27	4.	₹	12	5535	55356 NF093G10
1.7	823	4	ഹ	12	4901	19019 NF003H05
18	822	4,	വ	12	5769	57694 NF106E11
19	822	4.	o	12	9699	56953 NF098A09
20	820	4.	L)	10	1162	11625 NF065A04
21	w	4.	വ	10	4119	11795 NF067E07
22	18	4.	9	12	73	57321 NF1
23	816.5	4.	4	12	1984	19843 NF053G02
24	815	ᅻ.	∞	10	1130	11307 NF051D04
25	808	'n.	ഥ	10	3916	19165 NF094A12
26	ω :	Ë.	ഹ	12	5349	3495 NF086E02
27	800.5	·.	ഗ	13	1636	16365 NF047F08
28	_	<u>.</u>	S.	12	5522	5221 NF103D10
29	793.5	<u>.</u>	m	12	126509	5090 NF004G07
30	N I	m.	ຕ	12	126575	35759 NF093F11
31	-	<u>.</u>	മ	12	127133	1332 NF020D12
32	787.5	m.	~~	12	126638	6386 NF094A07
55.	82	'n.	\circ	12	126611	6110 NF085G04
λ. 4. ι	785	~ .	മം	13	3690	16907 NF020A12
22	183		~ ∨	7.0	F63904	19043 NF094G05
γ, ι	783		₩	10	E32234	2347 NF022G10
C 37		. i	₩ 1	13	016519	5195 EST61106
38	781.5	ď	\circ	12	358208	12080 EST48381
39	770	ď	_	12	290	2902 NF098G09
40	770	ď	\sim	12	126768	7682 NF111F08
41	770	٠.	\sim	10	F64243	2432 NF063E04
42	168	å	m	10	E32287	2878 NF048H12
43	166	٠: د	_	12	126770	267700 NF113G12
44	7	٠: د	α	13	25529	2255293 MTNAF12T
45	763.5	٠.	\sim		E32210	E322109 NF010B12

ALIGNMENTS

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/note="Vector: pBluescript SK -; Site 1: EcoRI; Site 2: XhoI; cDNA was prepared from polyA+ enriched RNA. The cDNA was directionally ligated into the Unizap XR vector from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DUO44449 745 bp MRNA linear EST 24-APR-2001
EST506108 KV3 Medicago truncatula cDNA clone pKV3-37M24 5' end,
MRNA Sequence.
                                                                                                                                                                                                           548
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129 AlaThrAlaGlyLeuArgLeuLeuAsnGlyAspAlaAlaGluLysIleLeuGlnAlaThr 148
                                                                                                                           488
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/tissue_type="Seedling roots"
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meliloti"
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                                                                                                                                                                                          369 GCAACCGCAGGTTTAAGGCTTTTGAATGGGGATGCTTCTGAAAAGATATTGCAAGCGGTA
                                                                                                                                                                                                                                                                              tThrTyrAlaValSerLysLysThrAlaLysAsnAlaProLysValAlaAspGlyGluAs
                                                                                    149 ArgAsnMetPheSerAsnArgSerThrLeuAsnValGlnArgAspAlaValSerllelle
                                                                                                          189 GlyLysSerPheThrLysSerValGlyValIleAspLeuGly-GlyGlySerValGlnMe
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1 (bases 1 to 745)

vandenBosch, K., Endre, G., Hur, J., Beremand, P., Town, C.D.,

bowman, C.L., Craven, M.B., Cho, J. and Fraser, C.M.

ESTS from roots of Medicago truncatula 72 h after Rhizobium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                M392896e TIGR sequence name: MTEBP84TK More information is available at: www.medicago.org Seq primer: SKmod (CTA gAA CTA gtg gAT CC). Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rLeuArgPheGlyLysGluAlaThrArgAla 258
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University of Minnesota
220 BioSci Center, 1445 Gortner Ave,
Tel: 612 624 2755
Fax: 612 625 1738
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/cultivar="genotype A17"
/db_xref="taxon:3880"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: kvandenb@cbs.umn.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone lib="KV3"
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Unpublished (2001)
Contact: VandenBosch K
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/organism="Medicago truncatula/Glomus versiforme mixed EST
library"
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//clone lib="MGHA"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
Xhol; cDNA was prepared from poly4+ enriched RNA from
roots harvested at 10, 17, 22, 31 and 38 days
post-inoculation with Glomus versiforme. The cDNA was
directionally ligated into the Unizap XR vector from
Stratagene and packaged using Giappeck III Gold packaging
extracts. Plasmids containing cDNA inserts were excised
from the recombinant lambda-Zap phage using Ex-assist
helper phage and propagated in XLOLR cells."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="roots colonized with Glomus versiforme" /dev stage="Roots harvested at 10, 17, 22, 31 and 38 days bost-incoculation with Glomus versiforme. The library was made from a mixture of RNA from each of these stages." /lab_host="E. coli strain XLOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            69 TTAGGAAACAACCTACTCACTCAATCGAAAGATTTTCCAAAAACAAGAAAATTTCCTCT 128
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                       ESTs from roots of Medicago truncatula after colonization with Glomus versiforme, 2001
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  type="roots colonized with Glomus versiforme"
                                                                                        Contact: Harrison M.J.
Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73401
Tel: 580-221-7380
Rax: 580-221-7380
Noble EST name: N379883e TIGR sequence name: MTDBQ16TK More information is available at: http://www.medicago.org
Seq primer: SKmod (CTA gAA CTA gtg gAT CC).
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="mRNA"
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/clone="pMHAM-15D7"
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EST611063 KVKC Medicago truncatula cDNA clone pKVKC-6G5, mRNA
sequence.
Stratagene and packaged using Gigapack III Gold packaging
extracts. Plasmids containing ofbM inserts were excised
from the recombinant lambda-Zap phage using Ex-assist
helper phage and propagated in XLOLR cells.
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                                                                                                                                                                                                            39 IlePheGlnLysGlnGluThr-LeuThrSerTyrAlaValIlePheAspAlaGlySerTh
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                                                                                                                                                                                                                                                                                                                                                                 180 AGATGTTGARGATATAAGACAACGCCCGGTTTGAGTGCATACGCGGATAATCCAGA
                                                                                                                                                                                                                                                                                                                                                                                                                   pleuHisProlysThrProLeuArgleuGlyAlaThrAlaGlyLeuArgleuLeuAsnGl
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        pValThrValAsnTyrValLeuGlyAsnLeuGlyLysSerPheThrLysSerValGlyVa

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                                                                                  3.79e-101
1000.50
89.92%
79.44%
                                                                                                                                                                     US-09-657-631-4 (1-459)
                                                                                                                     Best Local Similarity:
Query Match:
                                                                                                           Percent Similarity:
                                                                          Scores:
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DEFINITION
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/clone_libe_wKVKC"

/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
XhoI; cDNA was prepared from polyA+ enriched RNA. The cDNA
was directionally ligated into the Unizap XR vector from
Stratagene and packaged using Gigapack III Gold packaging
extracts. Plasmids containing cDNA inserts were excised
from the recombinant lambda-Zap phage using Ex-assist
helper phage and propagated in XLOLR cells."
                                                                                  Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids I; Fabales, Fabaceae, Papilionoideae, Trifolieae,
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                                                                                                                                                                                          Van Aken, S.
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                                                                                                                                                                                                                                                                                                                                                             55108,
                                                                                                                                        Medicago.

(Dases 1 to 743)

VandenBosch,K., Endere,G., Silverstein,K, Town,C.D., Van Utterback,T., Cheung,F. and Fraser,C.M.

The Medicago truncatula 'kiloclone' set; ESTs selected Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                          Tel: 612 624 2755
Fax: 612 625 1738
Email: kvandenbecbs.umm.edu
TIGR sequence name: WINAP77TK Alias Clone name: KV2-6L1
information is avvallable at: www.medicago.org
Seq primer: SKmod (CTA gAA CTA gtg gAT CC).
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                             Paul, MN
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1199
222
44
3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Medicago truncatula"
/mol type="mRNA"
/cultivar="A17"
/db xref="taxon:3880"
/clone="pKVKC-6G5"
/fisue_type="mixed tissues"
/dev stage="various stages"
/lab_host="XLOLR"
                                                                                                                                                                                                                                                                                                             Department of Plant Biology
University of Minnesota
220 BioSci Center, 1445 Gortner Ave, St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative:
Mismatches:
Indels:
                                                                                Eukaryota; Viridiplantae; Streptophyta;
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Matches:
                                         Medicago truncatula (barrel medic)
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  GI:20307369
                                                                                                                                                                                                                                                                                            Contact: VandenBosch K
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                                                              truncatula
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41.59%
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BI267324 651 bp mRNA linear EST 18-JUL-2001
NF105B12IN1F1101 Insect herbivory Medicago truncatula cDNA clone
NF105B12IN 5', mRNA sequence.
                                                                /note="Vector: pBluescript SK -; Site_1: EcoRI; Site_2:
Xho1; cDNA was prepared from polyA+ enriched RNA. The cDNA
was directionally ligated into the Unizap XR vector from
Stratagene and packaged using Gigapack III Gold packaging
extracts. Plasmids containing cDNA inserts were excised
from the recombinant lambda-Zap phage using Ex-assist
helper phage and propagated in XLOLR cells."
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/dev stage="24 hours post-inoculation with Sinorhizobium
meliToti"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  421 ACATATTCAGGAGTGGAGTACAAGGCTTTTTCCCCTTCTTCTGGCTCAAACTTTAATGAA
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178
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Mismatches:
Indels:
                                       /lab host="E. coli strain XLOLR"
/clone_lib="KV1"
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Matches:
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Medicago truncatula
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ORGANISM
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DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Texas A&M University name: T267654e TIGR sequence name: MTIAX42TK
More information is available at: http://chrysie.tamu.edu/medicago
Seq primer: SKmod (CTA gAA CTA gtg gAT CC).
Location/Qualifiers
1. 556
                                                                                                                                                                                                                                                                                                                                                                                       223
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
Spermatophyta, Magnoliophyta, Fabaceae, Papilionoideae, Trifolieae,
rosids, eurosids I, Fabales, Fabaceae, Papilionoideae, Trifolieae,
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Town,C.D., Bowman,C.L., Craven,M.B., Hansen,T.S., Holt,I.E. and
Fraser,C.M.
                                                                                                                                                                                  163
                                                                                                                                                                                                                   473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BSTS from roots of Medicago truncatula 24 hours after inoculation with Sinorhizobium meliloti
Unpublished (1999)
Contact: VandenBosch K
Department of Plant Biology
University of Minnesota
220 Biocsi Center, 1445 Gortner Ave, St. Paul, MN 55108, USA
                                            123
                                                                              353
                                                                                                                ProLeuArgLeuGlyAlaThrAlaGlyLeuArgLeuLeuAsnGlyAspAlaAlaGluLys 143
                                                                                                                                                  413
            293
                                                                                                                                  GlySerValGlnMetThrTyrAlaValSerLysLysThrAlaLysAsnAlaProLysVal
                                          Leulle ProLeuleu Gludladladluds pyal Val ProGluds pLeu His ProLysThr
                                                                                                                                                                                    IleLeuGlnalaThrArgAsnMetPheSerAsnArgSerThrLeuAsnValGlnArgAsp
                                                                                                                                                                                                                                                     AlaValSerIleIleAspGlyThrGlnGluGlySerTyrMetTrpValThrValAsnTyr
                                                                                                                                                                                                                                                                                                                       184 ValLeuGlyAsnLeuGlyLysSerPheThrLysSerValGlyValIleAspLeuGlyGly
                                                                                                                                                                                                                                                                                                                                                       534 GCATTGGGGGAAATTGGGAAAAATTCACAAAAACAGTGGGAGTAATGGATCTTGGAGGT
          AATAAGACAACGCCCGGTTTGAGTGCATACGCGGATAATCCAGAAGAAGCTGCAAAATCT
                                                                            294 TIGATICCACITITAGAGCAAGCAGAAAGIGIAGITICCIGAGGAICAGCGCTCCAAGACA
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/mol_type="mRNR"
/culfivar="genotype A17"
/du xref="taxon:3880"
/clone="pKV1-13H12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="Seedling roots"
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Fax: 612 625 1738
Email: kvandenb@ck
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BF003844.1
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Conservative:
Mismatches:
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University of Minnesota
220 BioSci Center, 1445 Gortner Ave,
Tel: 612 624 2755
Fax: 612 625 1738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="mixed tissues"
/dev_stage="various stages"
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/clone="pKVKC-12G8"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="mRNA"
/cultivar="A17"
                                                                                                                                                                                                                                                                                                                                                                                           BQ255419
BQ255419.1 GI:20456172
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BQ255419
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                                                                            Korth, K., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J., Flores, H.R., Inman, J.T., Weller, J.W. and May, G.D. Flores, H.R., Inman, J.T., Weller, J.W. and May, G.D. Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula insect herbivory library Contact. Korth K Contact. Korth K Dept. of Plant Pathology University of Arkansas 217 Plant Science Building, Fayetteville, AR 72701, USA Tel. 501 575 5191
Fax: 501 575 7601
Email: Korth@comp.uark.edu Insert Length: 651 Std Error: 0.00
Plate: 105 row: B Column: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /dry_subsect harbivory"
/clone lib="Insect herbivory"
/note="Vector: Lambda Zap; Library was produced from fully
sypanded M. truncatula leaves of plants fed upon by
Spodoptera exigua (beet armyworm) for 24 hours. Systemic
(undamaged leaves from injured plants) and wounded leaves
were harvested and pooled."
                  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
 Embryophyta; Tracheophyta;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62 GCTGGTAGCACCCTGGAAGCCGTGTCCATGTTACCATTTTGATCAAAACCTTAAAATCTTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       122 TCATGTTGGTAAAGATGTTGAGTTTTATAATAAGACAACGCCCGGTTTGAGTGCATACGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              114 lValProGluAspLeuHisProLysThrProLeuArgLeuGlyAlaThrAlaGlyLeuAr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        uHisIleGlyAsnAspIleGluPheValAspLysIleLysProGlyLeuSerAlaTyrGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  182 GGATAATCCAGAAGAAGCTGCAAAAACTTTTGATTCCACTTTTAGAGCAAGAAAGTGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="NF105B121N"
/tissue_type="local and systemic leaves"
/dev_stage="mature"
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Mismatches:
Indels:
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/mol_type="mRNA"
/db xref="taxon:3880"
Eukaryota; Viridiplantae; Streptophyta;
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Matches:
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Seq primer: TCACACAGGAAACAGCTATGAC.
Location/Qualifiers
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Best Local Similarity:
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/clone_TVEVEC.
/clone_TVEVEC.
/note=TVECTOR: BBluescript SK-; Site 1: EcoRI; Site 2:
XhoI; CDNA was prepared from polyA+ enriched RNA. The cDNA
was directionally ligated into the Unizap XR vector from
Stratagene and packaged using Gigapack III Gold packaging
extracts. Plasmids containing cDNA inserts were excised
from the recombinant lambda-Zap phage using Ex-assist
helper phage and propagated in XLOLR cells."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EST 06-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 735)
VandenBosch,K., Endre,G., Silverstein,K., Town,C.D., Van Aken,S.,
Utterback,T., Cheung,F., Fraser,C.M., Lamblin,A.-F. and Retzel,E.F.
The Medicago truncatula 'kiloclone' set; A selection of ESTs from
Various libraries rearrayed for gene expression studies
Unpublished (2002)
                                                                           481
                                                                                                                                                                                                                                                                                  234
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                                                                                                                                                                                                                                                                                                                                                   601
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This sequence represents the 5' end of the cDNA insert. More
information is available at: www.medicago.org
Seq primer: 5'gGC TCT AgA ACT AGT ggA TC 3'.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BQ255419 735 bp mRNA linear EST 06-MAY-;
MTNAL80TKW KVKC Medicago truncatula cDNA clone pKVKC-12G8, mRNA
174 ySerTyrMetTrpValThrValAsnTyrValLeuGlyAsnLeuGlyLysSerPheThrLy
                                    214 sLysThrAlaLysAsnAlaProLysValAlaAspGlyGluAspProTyrIleLysLysLe
                                                                                                                                                                                                                                                                                                                          542 GTATACAGCTAAAAATGCTCCAAAAGTTGCTGATGGAGAAGATCCATACATTAAGAAGCT
                                                                                                                                  194 sSerValGlyValIleAspLeuGlyGlyGlySerValGlnMetThrTyrAlaValSerLy
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                                                                                                                                                                                                                                                                                                                                                                                                                 234 uValLeuLysGlyLysGlnTyrAspLeuTyrValHisSerTyrLeu 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                            602 IGTACTCAAGGGAAAAAATATGATCTCTATGTTCATAGTTACTTA 647
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/organism="Medicago truncatula"
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COMMENT Contact: Harrison MJ Plant Biology Division The Samuel Roberts Noble Foundation 2510 Sam Noble Parkway, Ardmore, OK 73402, USA Tel: 580 221 7325	F : T : 580	/organism="Medicago riuncatura" /mol type="mRNA" /db xref="taxon:3880" /clone="NR038F11Pb" /tissue_type="leaf"	/dev_stage="trifoliate" /clone_lib="Phosphate starved leaf" /note="Vector: Landa Zap; At the trifoliate stage, M. /note="Vector: Landa Zap; At the trifoliate stage, M. /note="Vector: Landa Zap; At the trifoliate stage, M. /note="Vector: Landa Zap; At the phate standard to phosphate-free sand and grown for a further 30 days. During this 30 day period, the plants were fertilized twice weekly with 1/2 Hoaglands solution containing only 20M potassium.	phosphate. And was prepared from above grown of the state of the similarity: 89.57% Conservative: 23 the state of the similarity: 78.67% Manatches: 0.00cal Similarity: 78.67% Manatches: 0.00cal Similarity: 78.67% Manatches: 0.00cal Similarity: 0.	Gaps: Gaps: 04 (1-658)	Qy 88 ProGlyLeuSerAlaTyrGlyAspAsnProGluGlnAlaAlaLysSerLeuIleProLeu 107	Oy 108 ieuGluGluAlaGluAspValValProGluAspLeuHisProLysThrProLeuArgLeu 127	Qy 128 GlyAlaThrAlaGlyLeuLeuAsnGlyAspAlaAlaGluLysIleLeuGlnAla 147		31 20 22 22 43 24	Db 436 GATCCATACATTAAGAAGCTTGTACTCAAGGGAAAAATATGATCTTTTTTTATAGT 495 Cy 248 TYTLeuargPheGlyLysGlualaThrargalaGlnValleuAsnalaThrasnGlySer 267 Cy 248 TYTLeuargPheGlyLysGlualaThrargalaGlnValleuAsnalaThrasnGlySer 267
Query Match: 37.08% Indels: 0 DB: 13 Gaps: 0 US-09-657-631-4 (1-459) x BQ255419 (1-735)	Oy 1 GInIleLysAsnMetGluPheLeuIleThrLeuIleAlaThrPheLeuLeuLeuMet 20	41 G	Oy 61 ArgValHisValTyrHisPheAspGlnAsnLeuAspLeuLeuHisIleGlyAsnAspIle 80	Oy 101 AlaLysSerLeuIleProLeuLeuGludluAlaGluAspValValProGluAspLeuHis 120	Oy 141 AlaGluLysIleLeuGlnAlaThrArgAsnMetPheSerAsnArgSerThrLeuAsnVal 160 :::	Qy 161 GlnArgAspAlaValSerIleIleAspGlyThrGlnGluGlySerTyrMetTrpValThr 180 Db 541 CAACCTGAIGCAGTTTCTATTATTGAIGGAACCCAAGAAGGTTCTTATCTCTGGGTGAAC 600	Qy 181 ValasnTyrValleuGlyAsnLeuGlyLysSerPheThrLysSerValGlyVallleAsp 200	Qy 201 LeuGlyGlyGlySerValGlnMetThrTyrAlaValSerLysLysThrAlaLysAsnAla 220	Qy 221 ProLysValalaAsp 225 Db 721 NNNNAANNTGCTGAT 735	RESULT 7 B1263104 LOCUS B1263104 B1263104 LOCUS B1263104 B1263104 Clone NF038F11PL1F1095 Phosphate starved leaf Medicago truncatula cDNA CLOSSION B1263104 B	REFERENCE Medicago 1 to 658) AUTHORS Liu,J., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J., FOres,H.R., Imman,J.T., Weller,J.W., May,G.D. and Harrison,M.J. TILLE Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula phosphate-starved leaf library

300 254

SOURCE ORGANISM

AUTHORS

TITLE

REFERENCE

JOURNAL

COMMENT

LOCUS DEFINITION

BI270380 RESULT 8

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ACCESSION

VERSION KEYWORDS

274

314

651

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AW584590 657 bp mRNA linear BST 07-SBP-2000 N210666e MHAM Medicago truncatula/Glomus versiforme mixed BST library cDNA clone MHAM-2P11, mRNA sequence.
                                                                                                61 AGAAGTACCTTCAATGTTCAACCTGATGCAGTTTCTATTATTGATGGAACCCAAGAAGGT 120
                                                                  ArgSerThrLeuAsnValGlnArgAspAlaValSerIleIleAspGlyThrGlnGluGly 174
                                                                                                                                                   SerTyrMetTrpValThrValAsnTyrValLeuGlyAsnLeuGlyLysSerPheThrLys 194
                                                                                                                                                                         Fax: 580-221-7380
Email: mjharrison@noble.org
Other name: MHAM-2c-H06; Date: 3/14/00; Updated to the Database of
Expressed Sequence Tags (dbEST) on 04/27/00; More information is
available at _http://chrysie.tamu.edu/medicago'.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CysProTyrProSerCysThrPheGlyGlyIleTrpAsnGlyGlyGlyGlySerGlyGln 334
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1 (bases 1 to 65 EST libraries.

Harrison, M.J., Liu, J., Peng, H., Gonzales, M., Ellis, L., Town, C.D. Bowman, C.L., Craven, M.B., Hansen, T.S., Holt, I.E. and Fraser, C.M. ESTS from roots of Medicago truncatula after colonization with
    241 TATACAGCTAAAAATGCTCCAAAAGTTGCTGATGGAGAAGATCCATACATTAAGAAGCTT
                                                                                                                                                                                                                                                                                                                                                                                                 ValleuLysGlyLysGlnTyrAspLeuTyrValHisSerTyrLeuArgPheGlyLysGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              255 AlaThrArgAlaGlnValLeuAsnAlaThrAsnGlySerAlaAsnProCysIleLeuPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               275 GlyPheAsnGlyThrPheThrTyrSerGlyValGluTyrLysAlaPheSerProSerSer
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                                                                                                                                                                                                                                                                                                               215 LysThrAlaLysAsnAlaProLysValAlaAspGlyGluAspProTyrIleLysLysLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          335 LysLysLeuPheValThrSerAlaPheAlaTyrLeuAlaGluAspValGly 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        601 AGAATACTTTTTGCTGCTTCATCTTTTTTTTTTCCTANCTGAAGATATTGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2510 Sam Noble Parkway, Ardmore, OK 73401
Tel: 580-223-5810
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Plant Biology Division
The Samuel Roberts Noble Foundation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
1. .657
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seq primer: T3.
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VERSION
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AW584590
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SOURCE
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//issue_type="Developing flowers"
//dev_stage="Developing, fully-opened flowers and flowers
//dev_stage="Developing, fully-opened flowers and flowers
in early transition into pods."
//clone_lib="Developing, fully-opened flowers and flowers
in early transition into pods."
//clone_lib="Developing, fully-opened from polyA+
//note="Vector: Lambda Zap; cDNA was prepared from polyA+
//note="Vector: Lambda Zap; cDNA was prepared flowers and
flowers transitioning into pods. The cDNA was
directionally ligated into the Uni-Zap XR vector
(Stratagene) and packaged using the digapack III Gold
packaging extracts. Phagemids containing cDNA inserts were
using extasist helper phage and the E. coli strain
XLI-Blue WRRY (Stratagene). Excised plasmids were plated
using SOLR cells."
                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 652)

Torres-Jerez,I., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J., Flores,H.R., Imman,J.T., Weller,J.W. and May,G.D.

Expressed Sequence Tags from the Samuel Roberts Noble Foundation Unpublished (2001)
                                                                                                                                                                                                           EST 18-JUL-2001
                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
268 AlaAsnProCysIleLeuProGlyPheAsnGlyThrPheThrTyrSerGlyValGluTyr 287
                                                                                                                                                                                     652 bp mRNA linear EST 18-JUL-200
NF010D11FL1F1094 Developing flower Medicago truncatula cDNA clone
NF010D11FL 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
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Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402,
TE1: 580 221 7391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Medicago truncatula"
                                                                                                  Email: gdmay@noble.org
Insert Length: 652 Std Error: 0.00
Plate: 010 row: D column: 11
Seg primer: TCACACAGGAAACACCTATGAC.
                                                                             288 LysAlaPheSerProSerSerGlySerAsnPhe
                                                                                                                                                                                                                                                                                                                            Medicago truncatula (barrel medic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="mRNA"
/db_xref="taxon:3880"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-657-631-4 (1-459) x BI270380 (1-652)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                          BI270380.1 GI:14877916
EST.
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869.00
86.64%
73.27%
36.45%
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source

FEATURES

135 LeuLeuAsnGlyAspAlaAlaGluLysIleLeuGlnAlaThrArgAsnMetPheSerAsn 154

Query Match: DB:

à

Pred. No.:

ORIGIN

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/tissue_type="Developing flowers"
/dev_stage="Developing flowers"
/dev_stage="Developing flowers"
/dev_stage="Developing fully-opened flowers and flowers in early transition into pods."
/clone lib="Developing flower"
/note="Vector: Lambda Zap; cDNA was prepared from polyA-enriched, pooled samples of equivalent amounts of total RNA from very young, developing, fully-opened flowers and flowers transitioning into pods. The CDNA was forctor directionally ligated into the Uni-Zap XR vector (Stratagene) and packaged using the Gigapack III Gold packaging extracts. Phagemids containing cDNA inserts were in vivo excised from the recombinant Uni-Zap XR vector using ExAssist helper phage and the E. coli strain XLI-Blue MRR* (Stratagene). Excised plasmids were plated using SOLR cells."
                                                                                                                                                                                                                                                                                                                                                                                                       Torres-Jerez,I., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J., Flores,H.R., Inman,J.T., Weller,J.W. and May,G.D.
Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula flower library
Unpublished (2001)
                                                                                                                       BQ148414 673 bp mRNA linear EST 24-APR-2002
NF068A12FL1F1097 Developing flower Medicago truncatula cDNA clone
                                                                                                                                                                                                                                                                              Medicago truncatula
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids 1, Fabales, Fabaceae, Papilionoideae, Trifolleae,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23 IleThrSerSerGlnTyrLeuGlyAsnAsn---LeuLeuThrAsnArgLysIlePheGln 41
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168
22
24
24
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The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402,
TTel: 580 221 7380
Fax: 580 221 7380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Medicago truncatula"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: gdmay@noble.org
Insert Length: 673 Std Error: 0.00
Plate: 068 row: A column: 12
Seg primer: TCACACAGGAAACAGCTATGAC.
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Matches:
                                                                                                                                                                                                                                                           Medicago truncatula (barrel medic)
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/db_xref="taxon:3880"
                                                                                                                                                                       NF068A12FL 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="NF068A12FL"
                                                                                                                                                                                                                  BQ148414.1 GI:20285473
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854.00
87.96%
77.78%
35.82%
                                                                                                                                                                                                                                                                                                                                                                     Medicago.
1 (bases 1 to 673)
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Best Local Similarity:
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201
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DB:
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                                                                                                                                                                                                                    VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                    DEFINITION
                                                                                    RESULT 10
BQ148414
                                                                                                                                                                                                ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                     AUTHORS
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                                                                                                                                                /dev stage="Roots harvested at 10, 17, 22, 31 and 38 days post-inoculation with Glomus versiforme. The library was made from a mixture of RNA from each of these stages."
/lab host="E. coll strain XLOLR"
/lone lib="WHAM"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
/hote="Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI; cDNA was prepared from polyA+ enriched RNA from roots harvested at 10, 17, 22, 31 and 38 days post-inoculation with Glomus versiforme. The cDNA was directionally lighted into the Unizap XR vector from Stratagene and packaged using Gigapack III Gold packaging extracts. Plasmids containing cDNA inserts were excised from the recombinant lambda-Zap phage using Ex-assist helper phage and propagated in XLOLR cells:"
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'organism="Medicago truncatula/Glomus versiforme mixed EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GlnArgAspAlaValSerIleIleAspGlyThrGlnGluGlySerTyrMetTrpValThr 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  55 AAAATTAAGGATTATGGAGTTCCTAATTACACTAATCACCACTGTTCTACTGTTAAIG 114
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                                                                                                                                  tissue_type="roots colonized with Glomus versiforme"
                                           /mol_type="mRNA"
/cultivar="Medicago truncatula genotype A17"
/db_xref="taxon:119092"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   657
166
21
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                clone="MHAM-2P11"
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93.03%
82.59%
36.20%
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Best Local Similarity:
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/tissue_rwojingthowers"
/tissue_rwojingthowers"
/dev_stage="Developing flowers"
/dev_stage="Developing, fully-opened flowers and flowers in early transition into pods."
/clone_lib="Developing flower"
/clone_lib="Developing flower"
/note="Wector: Lambda Zap; cDNA was prepared from polyA+enriched, pooled samples of equivalent amounts of total RNA from very young, developing, fully-opened flowers and flowers transitioning into pods. The cDNA was directionally ligated into the Uni_Zap XR vector (Stratagene) and packaged using the Gigapack III Gold packaging extracts. Phagemids containing cDNA inserts were using ExAssist helper phage and the B. coli strain XL-Blue MRF' (Stratagene). Excised plasmids were plated using SOLR cells."
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853.00
88.89%
77.78%
35.78%
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Torres-Jerez,I., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J., Flores,H.R., Inman,J.T., Weller,J.W. and May,G.D. Expressed Sequence Tags from the Samuel Roberts Noble Foundation Unpublished (2001)
Contact: May GD
205
                                                                                                                                                265
                                                                                                                                                                               101
                                                                                                                                                                                                            325
                                                                                                                                                                                                                                  LysSerLeulleProLeuLeuGluGluAlaGluAspValValProGluAspLeuHisPro 121
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids I, Fabales, Fabaceae, Papilionoideae, Trifolieae,
                                                      61
                                                                                                                  81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               625 bp mRNA linear EST 18-JUL-200
NF091F05FL1F1046 Developing flower Medicago truncatula cDNA clone
RT270000
                                                                 ValHisValTyrHisPheAspGlnAsnLeuAspLeuLeuHisIleGlyAsnAspIleGlu
                                                                                                                               82 PheValAspLysIleLysProGlyLeuSerAlaTyrGlyAspAsnProGluGlnAlaAla
                                                                                                                                                                                               266 TTTTATAATAAGACAACGCCCGGTTTGAGTGCATACGCGGATAATCCAGAAGAAGCTGCA
                                                                                                                                                                                                                                                                                              122 LysThrProLeuArgLeuGlyAlaThrAlaGlyLeuArgLeuLeuAsnGlyAspAlaAla
                                              LysGlnGluThrLeuThrSerTyrAlaValIlePheAspAlaGlySerThrGlyThrArg
                                                                                                                                                                                                                                                    506 CCTGATGCAGTTCTATTATTGATGGAACCCAAGAAGGTTCTTATCTCTGGGGGACAGTT
                                                                                                                                                                                                                                                                                                                                                                                                                      162 ArgAspAlaValSerIleIleAspGlyThrGlnGluGlySerTyrMetTrpValThrVal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: gdmay@noble.org
Insert Length: 625 Std Error: 0.00
Plate: 091 row: F column: 05
Seq primer: TCACAGGAAACAGCTATGAC.
Location/Qualifiers
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The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK
Tel: 580 221 7391
Fax: 580 221 7380
Email: gdmay@noble.org
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                                                                                                                                                                  95 AspAsnProGluGlnAlaAlaLysSerLeuIleProLeuLeuGluGluAlaGluAspVal
                                                                                                                                                    115 ValProGluAspLeuHisProLysThrProLeuArgLeuGlyAlaThrAlaGlyLeuArg
                                                                                                                                                                                                   135 LeuleuAsnGlyAspAlaAlaGluLysIleLeuGlnAlaThrArgAsnMetPheSerAsn
                                                                                                                    ArgSerThrLeuAsnValGlnArgAspAlaValSerIleIleAspGlyThrGlnGluGly
                                                                                                                                                                                                                                                                    ServalGlyvalIleAspLeuGlyGlyGlyServalGlnMetThrTyrAlavalSerLys
                                                                                                                                                                                                                                                                                                                                                            215 LysThrAlaLysAsnAlaProLysValAlaAspGlyGluAspProTyrIleLysLysLeu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   255 AlaThrArgalaGlnValLeuAsnAlaThrAsnGlySerAlaAsnProCysIleLeuPro
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161
23
23
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          Matches:
Conservative:
Mismatches:
Indels:
 Length:
                                                                                US-09-657-631-4 (1-459) x BI272922 (1-625)
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127

147

167 478

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           656 bp mRNA linear EST 18-JUL-2001
NF093B10IN1F1089 Insect herbivory Medicago truncatula cDNA clone
NF093B10IN 5', mRNA sequence.
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids I; Fabales, Fabaceae, Papilionoideae, Trifolieae,
                                                                                                                                                                                                                                                                                                                                   188 LeuglyLysSerPheThrLysSerValGlyValIleAspLeuGlyGlyGlySerValGln 207
                                                                                                                                                                                                                                                                                                                                                                                                            MetThrTyrAlaValSerLysLysThrAlaLysAsnAlaProLysValAlaAspGlyGlu 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         168 IleAspGlyThrGlnGluGlySerTyrMetTrpValThrValAsnTyrValLeuGlyAsn 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 656)
Scoth, K., Scott, J., Harris, A.R., Gonzales, R.A., Bell, C.J.,
Flores, H.R., Imman, J.T., Weller, J.W. and May, G.D.
Expressed Sequence Tags from the Samuel Roberts Noble Foundation
                                                                                                                                                                            128 GlyalaThralaGlyLeuargLeuLeuAsnGlyAspAlaAlaGluLysileLeuGlnAla
                                                                                                                                                                                                                                 148 ThrArgAsnMetPheSerAsnArgSerThrLeuAsnValGlnArgAspAlaValSerIle
                                                                                                                                                                                                                                                              88 ProGlyLeuSerAlaTyrGlyAspAsnProGluGlnAlaAlaLysSerLeuIleProLeu
                    LeuGluGluAlaGluAspValValProGluAspLeuHisProLeuArgLeu
                                                                                                 Contactions (2004)
Contacts of Plant Pathology
University of Arkansas
217 Plant Science Building, Fayetteville, AR 72701, USA
Tel: 501 575 5191
Fax: 501 575 7601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Medicago truncatula insect herbivory library
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1. .656
/organism="Medicago truncatula"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: kkorth@comp.uark.edu
Insert Length: 656 Std Brror: 0.0
Plate: 093 row: B column: 10
Seq primer: TCACAGGAAACAGCTATGAC.
Location/Qualifiers
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S Korth, K., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J.,
Flores, H.R., Inman, J.T., Weller, J.W. and May, G.D.
Flores, H.R., Inman, J.T., Weller, J.W. and May, G.D.
Expressed Sequence Tags from the Samuel Roberts Noble Foundation
Medicago truncatula insect herbivory library
L Unpublished (2000)
Contact: Korth K
Dept. of Plant Pathology
University of Arkansas
217 Plant Science Building, Fayetteville, AR 72701, USA
Tel: 501 575 5191
Fax: 501 575 7601
Email: kkorth@comp.uark.edu
Insert length: 664 Std Brror: 0.00
Plate: 004 row: G column: 100
Plate: 004 row: G column: 100
Plate: 100-cation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="local and systemic leaves"
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/dev_stage="mature"
/clone lib="Insect herbivory"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                59 TATCTTGGAAACAATATACTCACCAATCGTAAAATATTTCCAAACAAGAAACTCTAAACC 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EST 18-JUL-2001
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                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolleae;
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NF004G10IN1F1084 Insect herbivory Medicago truncatula CDNA clone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="mRNA"
/db_xref="taxon:3880"
                                                                                                             NF004G10IN 5', mRNA sequence.
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GluLysIleLeuGlnAlaThrArgAsnMetPheSerAsnArgSerThrLeuAsnValGln 161
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            He,X.-Z., Shadle,G., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J., Flores,H.R., Inman,J.T., Weller,J.W., May,G.D. and Dixon,R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                       /dev_stage="Pooled developmental"
/clone_lib="Developing stem"
/note="Vector: Lambda Zap; Contains a mixture of
                                                                                                                                                                                                                         Email: radixon@noble.org
Medicago Genome Initiative accession: MGI:S:16915
Insert Length: 660 Std Brror: 0.00
Plate: 0.55 row: F column: 11
Seq primer: TCACACAGGAAACAGCTATGAC.
Location/Qualifiers
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Tel: 580 221 7302
Fax: 580 221 7380
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/mol_type="mRNA"
/db_xref="taxon:3880"
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Plant Biology Division
The Samuel Roberts Noble Foundation
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Spodoptera exigua (beet armyworm) for 24 hours. Systemic (undamaged leaves from injured plants) and wounded leaves were harvested and pooled."
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195 SerValGlyVallleAspLeuGlyGlyGlySerValGlnMetThrTyrAlaValSerLys
                                                                                                                                      ValleuLysGlyLysGlnTyrAspLeuTyrValHisSerTyrLeuArgPheGlyLysGlu
                                                                                                                                                            255 AlaThrArgAlaGlnValLeuAsnAlaThrAsnGlySerAlaAsnProCysIleLeuPro
                     LysThrAlaLysAsnAlaProLysValAlaAspGlyGluAspProTyrIleLysLysLeu
                                                                                       GlyPheAsnGlyThrPheThrTyrSerGlyValGluTyrLysAlaPheSerProSerSer
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/dev_stage="trifoliate"
/dev_stage="trifoliate"
/done_lib="phosphate starved leaf"
/note="vector: Lambda Zap; At the trifoliate stage, M.
truncatula plants were transplanted to phosphate-free sand
and grown for a further 30 days. During this 30 day
period, the plants were fertilized twice weekly with 1/2
Hoaglands solution containing only 20uM poteassium
phosphate. RNA was prepared from above ground tissues."
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bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
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Liu, J., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J.,
Liu, J., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J.,
Flores, H.R., Inman, J.T., Weller, J.W., May, G.D. and Harrison, M.J.
Flores, H.R., Inman, J.T., Weller, J.W., May, G.D. and Harrison, M.J.
Medicago truncatula phosphate-starved leaf library
Unpublished (2000)
                                                                                                                                                                                                                                 NFIGGAGIPLIFICE Phosphate starved leaf Medicago truncatula cDNA BG457472
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                           504 CCTGATGCAGTTTCTATTATTGATGGAACCCCAAGAAGGTTCTTATCTCTGGGTGACAGTT
                                                                                                             564 AACTATGCATTGGGGAAATTGGGAAAAATTCACAAAAACAGTGGGAGTAATGGATCTT
       ArgaspalavalSerIlelleAspGlyThrGlnGluGlySerTyrMetTrpValThrVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Harrison MJ
Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OX 73402, USA
Fax: 580 221 7325
Fax: 580 221 7380
Email: mjharrison@noble.org
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                                                                                                                                                   202 GlyGlyGlySerValGlnMetThrTyrAlaValSer
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/db_xref="taxon:3880"
/clone="NF106A03PL"
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AUTHORS
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## Sequence 8, Application US/09129112

| Sequence 8, Application US/09129112
| Patent NO. 6465716;
| Patent NO. 6465716;
| APPLICANT: Etzler, Marilynn E. | APPLICANT: Etzler, Marilynn E. | APPLICANT: Marilynn E. | APPLICANT: Marilynn E. | APPLICANT: Marilynn E. | APPLICANT: Marilynn E. | APPLICANT: Marilynn E. | APPLICANT: Marilynn E. | APPLICANT: Marilynn E. | APPLICANT: Marilynn E. | APPLICANT: Marilynn E. | APPLICANT: Marilynn E. | APPLICANT: Marilynn E. | Marilynn E. | Marilynn E. | Marilynn E. | Marilynn Marilynn Marilynn E. | Marilynn E. | Marilynn E. | Marilynn Marilynn Marilynn Marilynn Marilynn Marilynn Marilynn Marilynn Marilynn Marilynn Marilynn Marilynn Marilynn Marilynn Marilynn Marilynn Marilynn Marilynn Marilynn Marilynn Marilynn Marilynn Marilynn Marilynn Marilynn Marilynn Marilynn Marilynn Marilynn Marilynn Marilynn Marilynn Marilynn Marilynn Marilynn Marilynn Marilynn Marilynn Marilynn Marilynn Marilynn Marilynn Marilynn Marilynn Marilynn Marilynn Marilynn Marilynn Marilynn Marilynn Marilynn Marilynn Marilynn Marilynn Marilynn Marilynn Marilynn Marilynn Marilynn Marilynn Marilynn Marilynn Marilynn Marilynn Marilynn Marilynn Marilynn Marilynn Marilynn Marilynn Marilynn Marilynn Marilynn Marilynn Marilynn Marilynn Marilynn Marilynn Marilynn Marilynn Marilynn Marilynn Marilynn Marilynn Marilynn Marilynn Marilynn Marilynn Marilynn Marilynn Marilynn Marilynn Marilynn Marilynn Marilynn Marilynn Marilynn Marilynn Marilynn Marilynn Marilynn Marilynn Marilynn Marilynn Marilynn Marilynn Marilynn Marilynn Marilynn Marilynn Marilynn Marilynn Marilynn Marilynn Marilynn Marilynn Marilynn Marilynn Marilynn Marilynn Marilynn Marilynn Marilynn Marilynn Marilynn Marilynn Marilynn Marilynn Marilynn Marilynn Marilynn Marilynn Marilynn Marilynn Marilynn Marilynn Marilynn Marilynn Marilynn Marilynn Marilynn Marilynn Marilynn Marilynn Marilynn Marilynn Marilynn Marilynn Marilynn Marilynn Marilynn Marilynn Marilynn Marilynn Marilynn Marilynn Marilynn Marilynn Marilynn Marilynn Marilynn Marilynn Marilynn Marilynn Mar
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US-09-57-800C-2

US-09-240-639-5

US-09-240-639-5

US-09-370-265-6

US-09-370-265-6

US-09-370-265-6

US-09-370-265-6

US-09-557-800C-4

US-09-557-800C-48

US-09-557-800C-28

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Matches:
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OTHER INFORMATION: full length clone
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OTHER INFORMATION: NBP46
NAME/KEY: modified base
LOCATION: (1)...(1458)
OTHER INFORMATION: n = g, a, c
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TYPE: DNA ORGANISM: Medicago sativa
Percent Similarity:
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-LOOPEXT=0 -UNITS-bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE_FCT -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODEL_COAL_OUTPWIP=pto -NORMeext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=USO9657631_@CGN 1 1 76 @cunat 10082004 171046 £1692 -MCDU=6 -ICPU=3
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-NO_MMAP -LARGEQUERY -NEG SCORES=0 -MAIT - DSPELOCK=100 -LONGLOG
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-NO_MAP -LARGEQUERY -NEG SCORES=0 -MAIT - STARPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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/cgn2_6/ptodata/2/ina/fbZCOMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
          GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                         nucleic search, using frame_plus_p2n model
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US-09-129-112-18
US-09-129-112-3
US-09-350-858-4
US-09-370-265-4
US-09-370-265-4
US-09-557-800C-4
US-09-557-800C-4
US-09-557-800C-4
US-09-557-800C-4
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Listing first 45 summaries
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Database

Qy 341 SerAlaPheAlaTyrLeuAlaGluAspValGlyMetValGluProAsnLysProAsnSer 360	Db 1201 CTCTTATACCAACATGTCTTCTTCATGGATTTGGCTTAGGTCCACGAAAAGAGATT 1260 Qy	RESULT 2 US-09-129-112-13 Sequence 13, Application US/09129112 Sequence 13, Application US/09129112 Sequence 13, Application US/09129112 GENERAL INFORMATION: APPLICANT: Extler, Marilynn E. APPLICANT: Murphy, Judith B. APPLICANT: The Regents of the University of California TITLE OF INVENTION: A No. 6465716 Factor Binding Protein From Legume Roots FILE REPERENCE: 023907-079910US CURRENT PEPLICATION NUMBER: US/09/129,112 CURRENT FILING DATE: 1998-08-04	PRIOR APPLICATION NUMBER: US 08/907,226 PRIOR FILING DATE: 1997-08-06 NUMBER OF SEQ ID NOS: 19 SEQ ID NO 13 LENGTH: 1489 TYPE: DNA CREANISM: Lotus japonicus FEATURE: NAME/KEY: CDS LOCATION: (1)(1488)	JOCATION: (43)(1413) JOCATION: NBP46 J. OTHER INFORMATION: NBP46 J. OTHER INFORMATION: NBP46 Alignment Scores: 4.77e-196 Length: 1489 Pred. No.: 1665.50 Matches: 316 Score: 1665.50 Matches: 66 Percent Similarity: 68.70% Mismatches: 73 Query Match: 69.86% Mismatches: 5 DB: 10698: 4	US-09-657-631-4 (1-459) x US-09-129-112-13 (1-1489) QY
Leumet 	4 21 8 8	Leuhis Leuhis CTGCAC ASPAla GATGCT ASNVal	161 GlnargaspalaValSerIleIleAspGlyThrGlnGluGlySerTyrMetTr 181 CaaCGTGATGCATTTCTATTTGATGGAACCAAGAAGTTCTTTATTGIL 181 ValAsnTyrValLeuGlyAsnLeuGlyLysSerPhetThrLysSerValGlyVa 181 ValAsnTyrValLeuGlyAsnLeuGlyLysSerPhetThrLysSerValGlyVa 181 GTTAACTATGGGGAATTTGGGAAAAAGCTTCACAAAATCAGTGGGGTG 201 LeuGlyGlyGlyGrySerValGlnMetThrTyrAlaValSerLysLysThrAlaLy 1 [1	Oy 221 ProLysValAlaAspGlyGluAspProTyrIleLySLySLeuValLeuLySGlyLySGln 240	281 841 301 901 321

Db 1231 GATCTTGTCTACGTGTACACATTGCTTGTTGATG	Qy 420 IleThrValGlyGluGlyIleGlnTyrGlnAsnS.::	Qy 440 GlyThrAlaValGluAlaIleSerAlaLeuDroLy	RESULT 3 US-09-129-112-1 ; Sequence 1, Application US/09129112 ; Patent No. 6465716	GENERAL INFORMATION: APPLICANT: Etaler, Marilynn E. APPLICANT: Murphy, Judith B. APPLICANT: The Recents of the University	; TITLE OF INVENTION: A No. 6465716 Factor Bind; ; FILE REFERENCE: 023070-079810US ; CURRENT APPLICATION NUMBER: US/09/129,112 ; CURRENT FILING DATE: 1998-08-04	; PRIOR APPLICATION NUMBER: US 08/907,226 ; PRIOR FILING DATE: 1997-08-06 ; NUMBER OF SEQ ID NOS: 19 ; SOFFWARE: Patentin Ver 2 1	; SEQ ID NO 1 ; LENGTH: 1643 ; TYPE: DNA ; OTABALISM: Doliches biflorus	FEATURE: NAME/KEY: CDS LOCATION: (51)(1439) OTHER INFORMATION: NBP46 (NAME/KEY: mat_peptide LOCATION: (195)(1436) 5-09-129-112-1	Alignment Scores: Pred. No.: 1.3e-194 Length: Score: 1654.50 Marches: Percent Similarity: 82.75% Conservati		129-1 IleTh	Db 75 AGAGCATGAGCTTCCTACTCCTCATCAC Qy 23 IIAhrsersGinTyrLeuGlyAsnAsnLeule	Db 129 CTTTCTTCTCGCATATGTTGGGAACGGATCTT Qy 42 LysGlnGluThrLeuThrSerTyrAlaValllePh	Db 189 AACCAGGACTCCTTACCTTTACGCTGCTCTTCTTTTTTTT	Db 249 GTCHIGHTHING THE DD 249 GTCHIGHTHING THE DD 249 PheValAspLyshletysproglyleuseralaty.	Db 309 TTTACAAAAAAGATCCGGTTTGAGCTCATAAACQATTTGAGCTCTATAAACQATTTGAGCTCTATAAACQATTTGAGCTCTTGAGTTTGAGCTCATAAAAAAAAAA	Db 369 GAATCICICATICCACITITGGAGGAAGCTGAAGA Qy 122 LysThrProLeuArgLeuGlyAlaThrAlaGlyLe
154 AAAAATCAGGAACCAGTTACATCATAGGCTGTATATTTGATGCTGGTAGCACTGGAAGC 213	AspClnAsnLeuAspLeuLeuHislleGlyAsnAsplle 80	81 GluPheValAspLysIleLysProGlyLeuSerAlaTyrGlyAspAsnProGluGlnAla 100 	o ∧t	121 ProLysThrProLeuArgLeuGlyAlaThrAlaGlyLeuArgLeuLeuAsnGlyAspAla 140	141 AlaGluLysIleLeuGlnAlaThrArgAsnMetPheSerAsnArgSerThrLeuAsnVal 160 	161 GlnargAspalavalSerIleIleAspGlyThrGlnGluGlySerTyrMetTrpValThr 180 	181 ValasnTyrValLeuGlyAsnLeuGlyLysSerPheThrLysSerValGlyValIleAsp 200 	201 LeuglyGlySerValGlnMetThrTyrAlaValSerLysLysThrAlaLysAsnAla 220	221 ProlysValalaAspGlyGluAspProTyrIleLysLeuValLeuLysGlyLysGlyLysGln 240		261 LeuAsnAlaThrAsnGlySerAlaAsnProCysIleLeuProGlyPheAsnGlyThrPhe 280					1 lleLeuHisProValAspPheGluIleGlualaLysArgAlaCysAlaLeuAsnPheGlu		
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LysPheLysArgLeuMetTyrPhelle 459
GGATTTGGTCTTGATCCATTTCAAGAG 1290
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NAME/KEY: CDS
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                                                                                                       162 ArgAspAlaValSerIleIleAspGlyThrGlnGluGlySerTyrMetTrpValThrVal 181
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                                             GluLysIleLeuGlnAlaThrArgAsnMetPheSerAsnArgSerThrLeuAsnValGln 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   402 LeuTyrGlnHisValLeuLeuValHisGlyPheGlyLeuGlyProArgLysGluIleThr
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                                                                                                                                                                                     202 GlyGlyGlySerValGlnMetThrTyrAlaValSerLysLysThrAlaLysAsnAlaPro
                                                                                                                           LysvalalaaspGlyGluaspProTyrIleLysLysLeuValLeuLysGlyLysGlnTyr
                                                                           489 GAAAAGATATTGCAAGCGGTTAGGGAAATGTTCAGGAACAGAAGTTCCCTGAGCGTTCAA
442 AlaValGluAlaIleSerAlaLeuProLysPheLysArgLeuMetTyrPheIle 459
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US-09-129-112-18
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APPLICANT: Murphy, Judith B.
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: A No. 646516 Factor Binding Protein From Legume Roots
FILE REFERENCE: 023070-079810US
FILE REFERENCE: 023070-079810US
CURRENT APPLICATION NUMBER: US/09/129,112
CURRENT FILING DATE: 1998-08-04
PRIOR APPLICATION NUMBER: US 08/907,226
PRIOR FILING DATE: 1997-08-06
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 18
LENGTH: 1434 gene involved in oligosaccharide signaling LOCATION: (1133) ... (1151) OTHER INFORMATION: DBX9-for/rev primer LOCATION: [688]. [704]
OTHER INFORMATION: DBX2-for/rev primer NAME/KEY: primer bind LOCATION: Complement ((766). (785)) LOCATION: (297). (314)
OTHER INFORMATION: DBX7-for/rev primer NAME/KEY: primer_bind, LOCATION: (667). (685)
OTHER INFORMATION: DBX1-for/rev primer
NAME/KEY: primer bind NAME/KEY: primer_bind LOCATION: Complement((1075)..(1093)) OTHER INFORMATION: DEX11 primer LOCATION: (1414)...(1434) OTHER INFORMATION: DBXbottom primer NAME/KEY: primer_bind LOCATION: Complement((1)..(22)) OTHER INFORMATION: DBXtop primer OTHER INFORMATION: DBXS primer NAME/KEY: primer_bind LOCATION: (933)...(952) OTHER INFORMATION: DBX3 primer NAME/KEY: primer bind LOCATION: (955)...(972) LOCATION: (1227)...(1247)
OTHER INFORMATION: DBX12 primer INFORMATION: DEX10 primer NAME/KEY: misc feature LOCATION: (1071)..(1072) OTHER INFORMATION: splice site OTHER INFORMATION: DBXB primer NAME/KEY: primer bind LOCATION: (297) LOCATION: (856)..(857),
LOCATION: (856)..(857),
OTHER INFORMATION: splice site
NAME/KEY: primer_bind
NAME/KEY: primer_bind LOCATION: [955). (972)
OTHER INFORMATION: DBX4 primer primer ORGANISM: Dolichos biflorus LOCATION: (857). (872) OTHER INFORMATION: DBX6 | NAME/KEY: primer_bind LOCATION: (1)..(1404)
OTHER INFORMATION: DBX
NAME/KEY: sig_peptide
LOCATION: // NAME/KEY: misc feature LOCATION: (856)..(857) NAME/KEY: mat peptide LOCATION: (61)..(1404) (878) .. (896) NAME/KEY: primer_bind NAME/KEY: primer_bind LOCATION: (1133)..(11 NAME/KEY: primer bind US-09-129-112-18

Alignment Scores:

Sequence 18, Application US/09129112; Patent No. 6465716; GENERAL INFORMATION: APPLICANT: Etzler, Marilynn E.

us-09-657-631-4.p2n.rni

OW 314 ProCysProTyrProSerCysThrPheGlyGlylleTrpAsnGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyG	APPLICANT: The Regents of the University of California TITLE OF INNEWTHON's A. No. 646576 Factor Binding Protein From Legume Roots FILE REFERENCE: 023070-07981001 CURRENT APPLICATION WHERE: US/09/129,112 CURRENT FILING DATE: 1998-08-06 FRIOR PELING DATE: 1998-08-06 FRIOR PELING DATE: 1998-08-06 FRIOR PELING DATE: 1998-08-06 FRIOR FILING DATE: 1998-08-06 FRIOR FILING DATE: 1998-08-06 FRIOR FILING DATE: 1998-08-06 FRIOR FILING DATE: 1998-08-06 FRIOR FILING DATE: 1998-08-06 FRIOR FILING DATE: 1998-08-06 FRIOR FILING DATE: 1998-08-06 FRIOR FILING DATE: 1998-08-06 FRIOR FILING DATE: 1998-08-06 FRIOR FILING DATE: 1998-08-06 FRIOR FILING DATE: 1998-08-06 FRIOR FILING DATE: 1998-08-06 FRIOR FILING DATE: 1998-08-06 FRIOR FILING DATE: 1998-08-06 FRIOR FILING DATE: 1998-08-06 FRIOR FILING DATE: 1998-08-06 FRIOR FILING DATE: 1998-08-06 FRIOR FILING DATE: 1998-08-08-08-08-08-08-08-08-08-08-08-08-08
ore: rcent Sist Local sst Local : -09-657-	92 4 AGGCAATTGGAAGGGGATGCTTCCAACAGAGCGGTAAGTGGTGGAAG 483 94 AAAGAAGGAACATTGAAGGTTGGGGGATTCATTGCAAGCGGTAAGTGAAG 543 95 AAAGAAGCACATTGAAGGTTGGGGCGATTCATTTGATTGA

	173 GIUGLYSETIYIMETITDVAL	1832 AATTTTTTATAAGAAGATGGAAGAAGTGTGATCACATTACCTAGGACATTCATCTT 1891	1892 ATTTAAAATAATTTATTGCAAAATAATACTATTTTTTAATTAGAATTGATATTTGCGTAT 1951	ALTGTGAAAAAGAAAAGTAGATTGATTTTTCATTATGGTAAAGTATTTTAATAAATTTTT	179 179 2012 ATTAACTCTTTTAAAAATATAGGATCACTTTATGTGTGTG	179 179 2072 TACCCATATGACATGCCATACCCGATATTATTAATATTTTATGAATTGT 2131	179 179 2132 CAAITTATITATAAAACIACTTTAAAAATACTTTTAATTAA	179 179 2192 TTAGTTTTTTTTAAATTCGAAAAATAATTAATAATTATTAGATATACTGGAAGAATTT 2251	179 179		2312 AACACTAICTCTAAATAIGATTTTTTTTTTTTTTGTCGAATGAATCACGACGATATAATTT 2371	179		2432 AATTAGCTAAATCTTACCTAAAAAGATTGCAAACAAAGAAAAAAAA	1/3	179 179	2552 TATGTTTTCAAAAACTAGTAGTTGGAATTTCTTAAATTCAATTATAATTAAT	1/9	179 179 2672 TAITAAAAITTAITITIAIAGAIAAAAIGIAIITIGGIAAIAITIAIAAAAIAIT 2731	179
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Percent Similarity: 23.91% Conservative: 72 Best Local Similarity: 19.37% Mismatches: 74 Query Match: 41.88% Indels: 1133 DB: 4 Gaps: 11 US-09-657-631-4 (1-459) x US-09-129-112-3 (1-6265)	3 LysasnMetC ::: 699 AAGAGCATGA	23 IleThrSerSerGlnTyrLeuGlyAsnAsnLeuLeuThrAsnArgLysIlePheGln 41	42 LysGlnGluThrLeuThrSerTyrAlaValllePheAspAlaGlySerThrGlyThrArg 61	62 ValHisValTyrHisPheAspGlnAsnLeuAspLeuLeuHisIleGlyAsnAspIleGlu 81	PheValAspLys	933 TTTACAAAAAAGGTCAAACTGAAACCTTAAATTATTCATTATTATTTTTTTT	CTTACATTCTTCTTCTTATTCTGGTGCAGATCAAACCCGGTTTGAGCTCATACGCTGAT ASDProGluGlnAlaAlaLysSerLeulleProLeuLeuGluGluAlaGluAspValVal ::: :::	1053 AAGCCTGAAAAAGCTGCAGAATCTCTCATTTCGAGGAAGCTGAAGATGTTGTC 1112 116 ProGluAspLeuHisProLysThrProLeuArgLeuGly 128	1113 CCTGAGGAACTGCACCCCAAGACACCCCTTAAGCTTGGGGTGAGTATTTCTCATCTCTA 1172 128128	1173 TITTGCCACAGATTAATATGTCACACTTTTACATGAAACATGATTAAGTTCTTTAAACAT 1232	128 128 1233 GTTGATTAAAGGGTGACAGTTTGTATTTTTAATCAAGTAATCTAGAACTTAAACTATGG 1292		1293 TAATAATATAAAATGAATATGAAACTAATATATTCTGATGGAACAGAAGAAAGCAATATC 1352	128	128 128	AGACCAAATAAAATAGGCATTAGCCCATATCATAAAATCTTTTGTAAAATATTAATAGAA	128	AlaThrAlaGlyLeuArgLeuLeuAsnGlyAsp		1593 ĠĊTĠĊTĠĀĀĀĀĠĀŤŤĠĊĀĀĠĠĠŦPĀCCĀTĀGŦĠŦŢŦĊŢŢŦŢŦŢŦ 1652 148ThrāvgĀsnMetPhe 152

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AsnAspProCysProTyrProSerCysThrPheGlyGlyIleTrpAsnGlyGlyGlyGlyGly 331
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                                                                                                                                                                                                                                                                                                                                                                                                                             ValaspLyslleLysProGlyLeuSerAlaTyrGlyAspAsnProGluGlnAlaAlaLys 102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ThrProLeuArgLeuGlyAlaThrAlaGlyLeuArgLeuLeuAsnGlyAspAlaAlaGlu 142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         163 AspAlavalSerileIleAspGlyThrGlnGluGlySerTyrMetTrpValThrValAsn
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PheAspGln-----AsnLeuAspLeuLeuHisIleGlyAsnAspIleGluPhe
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143
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Mismatches:
Indels:
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                                                                                                                       Length:
Matches:
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507.50
49.41%
33.97%
21.29%
               ; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1284)
US-09-608-285A-4
                                                                                                                                                               Query Match:
                                                                                                                                                            Percent Similarity:
ORGANISM: HOMO
                                                                                                          Alignment Scores:
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APPLICANT: Ford, John
APPLICANT: Ford, John
APPLICANT: Wulero, Julio
APPLICANT: Found, George
TITLE OF INVENTION: POLYPEPTIDES
TITLE OF INVENTION: POLYPEPTIDES
TITLE OF INVENTION: POLYPEPTIDES
TITLE OF INVENTION NUMBER: US/09/608,285A
CURRENT APPLICATION NUMBER: US/09/608,285A
CURRENT APPLICATION NUMBER: 09/583,231
PRIOR APPLICATION NUMBER: 09/583,231
PRIOR FILING DATE: 2000-60-26
PRIOR FILING DATE: 2000-01-11
PRIOR APPLICATION NUMBER: 09/481,238
PRIOR FILING DATE: 1990-01-11
PRIOR APPLICATION NUMBER: 09/370,265
PRIOR FILING DATE: 1999-07-09
PRIOR FILING DATE: 1999-07-06
PRIOR FILING DATE: 1999-07-09
PRIOR FILING DATE: 1999-07-09
PRIOR FILING DATE: 1999-07-04
PRIOR APPLICATION NUMBER: 09/224,444
PRIOR FILING DATE: 1999-07-04
PRIOR PRILING DATE: 1999-07-04
PRIOR PRILING DATE: 1999-07-04
PRIOR PRILING DATE: 1999-07-04
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                                                                -AsnleuAspLeuLeuHisIleGlyAsnAspIleGluPhe 82
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307 ACCGTICAAGGGCTCTTAGAGGTGGCCAAAGACTCAATCCCCCGAAGTCACTGGAAAAG
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APPLICANT: Ford, John
APPLICANT: Ford, John
TITLE OF INVENTION:
FILE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE
FILE REFERENCE: 20110/35761
CURRENT APPLICATION NUMBER: U5/09/350,836B
PRIOR APPLICATION NUMBER: 09/118,205
PRIOR APPLICATION NUMBER: 09/118,205
PRIOR APPLICATION NUMBER: 09/118,205
PRIOR PLING DATE: 1999-07-16
PRIOR PLING DATE: 1998-07-16
PRIOR PLING DATE: 1998-07-16
PRIOR PLING DATE: 1998-07-24
PRIOR PLING DATE: 1998-07-24
PRIOR PLING DATE: 1998-07-24
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                                                  SerGlyGlnLysLysLeuPheValThrSerAlaPheAlaTyrLeu-----AlaGlu
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ORGANISM: Homo sapiens
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US-09-350-836B-4
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107 ACCGITICAAGGGCICITIAGAGGIGGCCAAAGACICAAICCCCCCGAAGICACIGGAAAAAG 366
                                                       ACCCCAGIGGICCIAAAAGCAACACCAGACIACGCIIACIGCCAGAACACAAAAGACAAAG 426
                                                                                     143 LysIleLeuGlnAlaThrArgAsnMetPheSerAsnArgSerThrLeuAsnValGlnArg 162
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                             ThrProLeuArgLeuGlyAlaThrAlaGlYLeuArgLeuLeuAsnGlyAspAlaAlaGlu
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APPLICANT: Ford, John
APPLICANT: Ford, John
APPLICANT: Ford, John
APPLICANT: Malero, Julio
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE
TITLE OF INVENTION: POLYPEPTIDES
FILE REPERENCE: 28111/35908
CURRENT FILING NAMER: U5/09/370,265
CURRENT FILING DATE: 1999-00-09
EARLIER APPLICATION NUMBER: DCT/US99/16180
EARLIER APPLICATION NUMBER: 09/350,836
EARLIER FILING DATE: 1999-07-09
EARLIER FILING DATE: 1999-07-09
EARLIER FILING DATE: 1999-02-04
EARLIER FILING DATE: 1999-02-04
EARLIER APPLICATION NUMBER: 09/122,44
EARLIER PLING DATE: 1999-02-04
EARLIER PLING DATE: 1999-02-04
EARLIER PLING DATE: 1999-02-04
EARLIER PLING DATE: 1999-07-24
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EARLIER PLING DATE: 1998-07-24
EARLIER PLING DATE: 1998-07-24
EARLIER PLING DATE: 1998-07-16
SOUTWARE: PALCATION NUMBER: 09/118,205
EARLIER PLING DATE: 1998-07-16
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Patent No. 6447771
GENERAL INFORMATION:
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GCTCTGCTCTTTGAGGTAAAGGAGATCTTC---AGGAAGTCACCTTTCCTGGTACCAAAG 483
                                                                        484 GCCAGTGTTAGCATCATGGATCCGACGAAGGCATATTAGCTTGGGTTACTGTGAAT 543
                                                                                                                                      -----GGCTACCTCCTTTGAGATGTTTAACAGCACTTAT 705
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                                163 AspAlaValSerIleIleAspGlyThrGlnGluGlySerTyrMetTrpValThrValAsn
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APPLICANT: Ford, John APPLICANT: Mulero, Julio
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TITLE OF INVENTION: Methods and Materials Relating to CD39-Like
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 28110/36457
CURRENT APPLICATION NUMBER: US/09/557,800C
CURRENT FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/481,238
PRIOR FILING DATE: 2000-01-11
PRIOR PELLING DATE: 1999-00-16
PRIOR FILING DATE: 1999-07-16
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                                            Sequence 4, Application US/09557800C
Patent No. 6476211
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21.29%
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SEQ ID NO 4
LENGTH: 1287
                                                                        GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Ford, John
APPLICANT: Mulero, Julio
APPLICANT: Yeung, George
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Best Local Similarity:
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; LOCATION: (1)
US-09-557-800C-4
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APPLICANT: Ford, John
APPLICANT: Wilero, Julio
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APPLICANT: Walero, Julio
APPLICANT: Walero, Julio
APPLICANT: Walero, Julio
APPLICANT: Yeung, George
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CD39-LIKE
TITLE OF INVENTION: POLYPEPTIDES
FILE REFERENCE: 28110/36570
CURRENT PAPLICATION NUMBER: 08/983,231
PRIOR APPLICATION NUMBER: 09/583,231
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-25
PRIOR PAPLICATION NUMBER: 09/481,238
PRIOR FILING DATE: 1999-00-11
PRIOR FILING DATE: 1999-00-09
PRIOR FILING DATE: 1999-07-16
PRIOR FILING DATE: 1999-07-16
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946 CACCAGCCAGAGGAGGTCCAGAGAGGTTCCTTC---
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           TITLE OF INVENTION: METHODS AND MATERIALS KELL
FILE REFERENCE: 28110/35908
CURRENT APPLICATION NUMBER: US/09/370,625A
CURRENT FILING DATE: 1999-08-09
PRIOR APPLICATION NUMBER: PCT/US99/16180
PRIOR FILING DATE: 1999-07-16
PRIOR APPLICATION NUMBER: 09/350,836
PRIOR APPLICATION NUMBER: 09/273,447
PRIOR APPLICATION NUMBER: 09/273,447
PRIOR FILING DATE: 1999-07-09
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PATENTIN VET: 2.0
SEQ ID NO 4
SEQ ID NO 4
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TYPE: DNA
ORGANISM: Homo sapiens
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1458 GTGAACAAC---ATAGAGACGGGCTGGGGCCTTTGGGGGGCCACTTTCACCTGTTGCAGTCT 1514
                                        -AlaAsnProCyslleLeuPro 274
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APPLICANT: Ford, John
APPLICANT: Ford, Julio
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE
TITLE OF INVENTION: POLYPEPTIDES
TITLE OF INVENTION: POLYPEPTIDES
TILE REFERENCE: 28110/35761
CURRENT APPLICATION NUMBER: U5/09/350,836B
CURRENT FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: 09/273,447
PRIOR APPLICATION NUMBER: 09/118,205
PRIOR PLING DATE: 1998-07-16
PRIOR APPLICATION NUMBER: 09/12,449
PRIOR PLING DATE: 1998-07-16
PRIOR PLING DATE: 1998-07-24
PRIOR PLING DATE: 1999-02-04
PRIOR PLING DATE: 1999-02-04
NUMBER: 09/244,444
                                                                                                        275 GlyPheAsnGlyThrPheThrTyrSerGlyValGluTyrLysAlaPheSerProSerSer
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                                  262 AsnAla-----ThrAsnGlySer-
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ORGANISM: Homo sapiens
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ORCANISM: Homo sapiens
ORCANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
I.OCATION: (246)..(1529)
NAME/KEY: misc feature
I.OCATION: (1718)
COCATION: (1718)
OTHER INFORMATION: n = adenine or guanine or cytosine or thymidine
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Matches:
Conservative:
Mismatches:
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| PRIOR APPLICATION NUMBER: 09/244,444 |
| PRIOR FILING DATE: 1999-02-04 |
| PRIOR PEDILCATION NUMBER: 09/122,449 |
| PRIOR FILING DATE: 1998-07-24 |
| PRIOR FILING DATE: 1998-07-16 |
| PRIOR FILING DATE: 1998-07-16 |
| NUMBER OF SEQ ID NOS: 60 |
| SOFTWARE: Patentin Ver. 2.0 |
| SEQ ID NO 2 |
| LENGTH: 1799 |
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1191 CACCAGCCAGAGGTCCAGAGGTTCCTTC	349 AspvalGlyMetValGluProAsnLysProAsnSerIleLeuHisProValAspPheGlu		Db 1407 AAGGATGGCTTTGGAGACAGGACACAGTCTTACAGAGAAA 1457 Qy 429 GlnAsnSerValValGluAlaAlaTrpProLeuGlyThrAlaValGluAlaIleSerAla 448 Db 1458 GTGAACAACATAGAGACGGGCTGGGGCCTTGGGGGCCACCTTTCACCTGTTGCAGTCT 1514	1515 CTG 1515 CTG SULT 13 -08-370-265-2	Sequence 2, Application US/09370265 Patent No. 6447771 APPLICANT: Ford, John APPLICANT: Mulero, Julio	TITLE OF INVENTION: METHADS AND MAIERIALS KELALING TO NOVEL COST-LINE TITLE OF INVENTION: POLYPEPTIDES TITLE OF INVENTION: POLYPEPTIDES TITLE OF INVENTION NUMBER: US/09/370,265 CURRENT APPLICATION NUMBER: US/09/370,265 CURRENT FILING DATE: 1999-08-009 TOTAL		APPLICATION N FILING DATE: APPLICATION N FILING DATE: APPLICATION N FILING DATE: PILING DATE:	; SOFTWARE: Patentin Ver. 2.0 ; SEQ ID NO 2 ; LENGTH: 1799 ; TYPE: DNA Pemo sapiens	(1529) feature 3)	GTHER INFORMATION: n = adenine or guanine or cytosine or thymine US-09-370-265-2 Alignment Scores: Pred. No.: Score: 507.50 Matches: 143
) LOCATION: (246)(1529)) NAME/KEY: misc feature) LOCATION: (1718)) OTHER INFORMATION: n = adenine or guanine or cytosine or thymine US-09-350-836B-2		-03-65/-631- 47 384		103 SerLeulleProLeuLeuGluGluAlaGluAspValValProGluAspLeuHisProLys:::::::	Oy 123 ThrProLeuArgleuGlyAlaThrAlaGlyLeuArgleuLeuAsnGlyAspAlaciu 142	Db 672 GCTCTGCTCTTTGAGGTRAAGGAGATCTTCAGGAAGTCACCTTTCCTGGTACCAAAG 728 Qy 163 AspalaValSerIleIleAspGlyThrGlnGluGlySerTyrMetTrpValThrValAsn 182 Db 729 GGCAGTGTTAGCATCATGGATGGATCGACGAAGGCATATAGCTTGGGTTACTGTGAAT 788	183		242 AspleuTyrValHisSerTyrLeuargPheGlyLysGl	262 AsnAlaIntrasnctySer	

Db 1257 GACACAGACATGATTATGAAAAGGGGGGTATTTTAAAAGTTGAAGATTTTGAA 1313 Qy		1407	OY 429 GlnAsnSerValValGluAlaAlaTrpProLeuGlyThrAlaValGluAlaIleSerAla 448	Qy 449 Leu 449 Db 1515 CTG 1517	RESULT 14 US-09-557-800C-2 ; Sequence 2, Application US/09557800C ; Patent No. 647621	; GENERAL INFORMATION: ; APPLICANT: Ford, John ; APPLICANT: Mulero, Julio ; APPLICANT: Yeung, George	NVENTION: NVENTION: ENCE: 281	CURRENT FILING DATE: 2000-04-25 PRIOR APPLICATION NUMBER: 09/481,238 PRIOR FILING DATE: 2000-01-11 PRIOR APPLICATION NUMBER: 09/370 965	PRIOR FILING DATE: 1999-06 PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 1999-07 PRIOR APPLICATION NUMBER:	; PRIOR FILING DATE: 1999-07-09; ; PRIOR APPLICATION NUMBER: 09/273447; PRIOR FILING DATE: 1999-03-19; PRIOR APPLICATION NUMBER: 09/122449	PRIOR FILING DATE: 1998-07 PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 1999-02 PRIOR APPLICATION NUMBER:	; PRIOR FILING DATE: 1998-07-16 ; NUMBER OF SEQ ID NOS: 56 ; SOFTWARE: Patentin Ver. 2.0 ; SEQ ID NO 2	; LENGTH: 1799 ; TYPB: DNA ; OGGANISM: Homo sapiens ; FEATURE:	NAME/KEY: CDS; LOCATION: (246)(1529) ; FEATURE: ; NAME/KEY: misc_feature	; DOCATION: (1718) ; OTHER INFORMATION: n = adenine or guanine or cytosine or thymidine US-09-557-800C-2	Alignment Scores: Pred. No.: Score: Score: Score: Series: Fercent Similarity: Score: Best Local Similarity: Cuery Match: DB: DB: DB: DB: DB: DB: DB: DB: DB: DB	. 4 Gaps:
Percent Similarity: 49.41% Conservative: 65 Best Local Similarity: 33.97% Mismatches: 152 Query Match: 21.29% Indels: 61 DB: 4 Gaps: 16 US-09-657-631-4 (1-459) x US-09-370-265-2 (1-1799)	ThrSerTyralaValilePh	67 PheAspGlnAsnLeuAspLeuLeuHislleGlyAsnAspIleGluPhe 82 	83 ValAspLysIleLysProGlyLeuSerAlaTyrGlyAspAsnProGluGlnAlaAlays 102 	103 SerLeulleProLeuLeuGluGluAlaGluAspvalValProGluAspLeuHisProLys 122 ::::::	123 ThrProLeuargLeuGlyalaThrAlaGlyLeuargLeuLeuasnGlyaspalaalaGlu 142 	143 LysIleLeuGlnAlaThrArgAsnMetPheSerAsnArgSerThrLeuAsnValGlnArg 162	163 AspalavalSerIleIleAspGlyThrGlnGluGlySerTyrMetTrpValThrValAsn 182 	183 TyrValLeuGlyAsnLeuGlyLysSerPheThrLysSerValGlyValIleAspLeuGly 202 	203 GlyGlySerValGlnMetThrTyrAlaValSerLysLysThrAlaLysAsnAlaPro 221	222 LysValAlaAspGlyGluAspProTyrIleLysLysLeuValLeuLysGlyLysGlnTyr 241 :: ::	242 AspleuTyrValHisSerTyrLeuArgPheGlyLysGluAlaThrArgAlaGlnValLeu 261 	262 AsnAlaThrAsnGlySerAlaAsnProCysIleLeuPro 274	275 GlyPheasnGlyThrPheThrTyrSerGlyValGluTyrLysalaPheSerProSerSer 294 ::: ::: :::	295 GlySerAsnPheAspAspCysLysGluIleIleLeuLysValLeuLysVal 311 ::: ::: 131 GGGAGGTGGGCTTTGAGCCCTGCTATGCCGAAGTGCTGAGGGTGGTACGAGGAAAACTT 1190	312 AsnAspProCysProTyrProSerCysThrPheGlyGlyIleTrpAsnGlyGlyGlyGly 331 ::: 1191 CACCAGAGAGGTCCAGAGAGGTTCCTTC	332 SerGlyGlnLysLysLeuPheValThrSerAlaPheAlaTyrLeuAlaGlu 348 1224TATGCTTTCTCTTACTATATGACCGAGCTGTT 1256 349 AspValGlyMetValGluProAsnLysProAsnSerIleLeuHisProValAspPheGlu 368	

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Sequence 2, Application US/09370625A; Patent No. 6600032; GENERAL INFORMATION:
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                                                                                                                                                 409 ValHisGlyPheGlyLeuGlyProArgLysGluIleThrValGlyGluGlyIleGlnTyr
                                                                                                                                                                                      LeuThrAspAlaLysArgProTyrValCysMetAspLeuLeuTyrGlnHisValLeuLeu
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NAME/KEY: CDS
LOCATION: (246)..(1529)
FEATURE:
NORME/KEY: misc_feature
LOCATION: (1718)
OTHER INFORMATION: n = adenine or guanine or cytosine or thymine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: POTATION
APPLICANT: MAIECA, John
APPLICANT: MAIECA, John
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD35
FILE REPERENCE: 28110/35908
CURRENT APPLICATION NUMBER: US/09/370,625A
CURRENT FILING DATE: 1999-08-09
PRIOR APPLICATION NUMBER: PGT/US99/16180
PRIOR PILING DATE: 1999-07-16
PRIOR PILING DATE: 1999-07-16
PRIOR PILING DATE: 1999-03-19
PRIOR FILING DATE: 1999-03-19
PRIOR FILING DATE: 1999-03-19
PRIOR FILING DATE: 1999-03-19
SOFTWARE: PARENTING DATE: 1999-03-19
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1314 AGAAAAGCCAGGGAAGTGTGAT---AACTTGGAAAACTTCACCTCA-
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Conservative:
Mismatches:
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	123 ThrProLeuArgLeuGlyAlaThrAlaGlyLeuArgLeuLeuAsnGlyAspAlaAlaGlu 142 ::	143 LysIleLeuGlnAlaThrArgAsnMetPheSerAsnArgSerThrLeuAsnValGlnArg 162 :::	163 AspalavalSerIleIleAspGlyThrGlnGluGlySerTyrMetTrpValThrValAsn 182 ::: ::		22	222 LysValAlaAspGlyGluAspProTyrIleLysLysLeuValLeuLysGlyLysGlnTyr 241	242 AspLeuTyrvalHisSerTyrLeuArgPheGlyLysGluAlaThrArgAlaGlnValLeu 261	262 AsnalaThrAsnGlySerAlaAsnProCysIleLeuPro 274	275 GlyPheAsnGlyThrPheThrTyrSerGlyValGluTyrLysAlaPheSerProSerSer 294 :::	295 GlySerAsnPheAspAspCysLysGluIleIleLeuLysValLeuLysVal 311	312 AsnaspProCysProTyrProSerCysThrPheGlyGlyIleTrpAsnGlyGlyGlyGly 331 :::	PhealaryrLeuAlaglu 34	349 AspvalGlyMetValGluProAsnLysProAsnSerIleLeuHisProValAspPheGlu 368	369 IleGluAlaLysArgAlaCysAlaLeuAsnPheGluAspValLysSerThrTyrProArg 388	HisValLeuLeu 40	409 ValhisGlyPheGlyLeuGlyProArgLysGlulleThrValGlyGluGlyIleGlnTyr 428	GlnAsnServalvalGluAlaAlaTrpProLeuGlyThrAlaValGluAlaIleSerAla ::: ::: GTGAACAACATAGAGACGGGCTGGGGCCTTGGGGGCCACCTTTCACCTGTTGCAGTCT	449 Leu 449
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Db 1515 CTG 1517

Search completed: August 19, 2004, 20:35:42 Job time : 114.192 secs

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Sequence 8, Appli Sequence 13, Appl Sequence 1, Appli Sequence 8688, Ap Sequence 2234, Ap Sequence 11084, Ap Sequence 11084, A

Title: Perfect score:

Sequence:

OM protein

Run on:

Scoring table:

Searched:

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APPLICANT: Etzler, Marilynn E.
APPLICANT: Etzler, Marilynn E.
APPLICANT: Murphy, Judith B.
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: A No. US2002019995A1 Factor Binding Protein From Legume Roots
FILE REFERENCE: 023070-0798100S
CURRENT APPLICATION NUMBER: US/09/129,112
CURRENT PELICATION NUMBER: US 08/907,226
PRIOR FILING DATE: 1997-08-06
NUMBER OF SEQ ID NOS: 19
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 8
                                                                                      3 US-10-12-13-18

3 US-10-425-112-18

3 US-10-425-114-11084

3 US-10-424-1888

1 US-09-938-842A-1888

1 US-09-938-842A-849

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8 US-10-286-926-526-6
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       1458
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3654.341 Million cell updates/sec
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                                                                                                                                                                                                         .......GTAVEAISALPKFKRLMYFI 459
                                                                                                  August 19, 2004, 15:09:55 ; Search time 616.984 Seconds
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                               nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                        3228839 seqs, 2456066551 residues
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Maximum Match 1008
Listing first 45 summaries
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Kgapop 10.0 , Kgapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
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Maximum DB seq length: 200000000
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Jatabase

Sequence 73, Appl.
Sequence 285, Appl.
Sequence 30,091,
Sequence 6144, Appl.
Sequence 89910, A
Sequence 89910, A
Sequence 119497,
Sequence 52833, A

Sequence 287, App Sequence 8398, Ap Sequence 123779, Sequence 4, Appli

Sequence Sequence S

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NAME/KEY: CDS LOCATION: (1)..(1458)

Description

Query Match Length DB

Score

Result

FEATURE:

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Sequence 849, App Sequence 849, App Sequence 29868, A

Sequence 1888, Ap Sequence 1888, Ap

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Sequence 13, Application US/09129112
| Sequence 13, Application US/09129112
| Sequence 13, Application US/09129112
| Sequence 10, Application US/09129112
| APPLICANT: Etzler, Marilynn B. APPLICANT: Murphy, Judith B. APPLICANT: The Regents of the University of California
| APPLICANT: The Regents of the University of California
| TITLE OF INVENTION: A No. US20020019995A1 Factor Binding Protein From Legume Roots
| FILE REFREENCE: 023070-079810US
| CURRENT APPLICATION NUMBER: US/09/129,112
| CURRENT FILING DATE: 1998-08-04
| PRIOR APPLICATION NUMBER: US 08/907,226
| PRIOR PILING DATE: 1997-08-06
| NUMBER OF SEQ ID NOS: 19
| SOFTWARE: Patentin Ver. 2.1
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                          CystysGlullelleLeuLysValLeuLysValAsnAspProCysProTyrProSerCys
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; OTHER INFORMATION: full le:
; NAME/KEY: CDS
; CCATION: (43)..(1413)
; OTHER INFORMATION: NBE46
US-09-129-112-13
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ValAsnTyrValLeuGlyAsnLeuGlyLysSerPheThrLysSerValGlyVallleAsp
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                                                                                                                                                1458
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Conservative:
Mismatches:
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          INFORMATION: full length
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100.00%
100.00%
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                                                                              LOCATION: (1)..(1458)
OTHER INFORMATION: n = g,
                                                OTHER INFORMATION: NBP46
NAME/KEY: modified base
                       NAME/KEY: CDS
LOCATION: (13)..(1380)
                                                                                                                                                                          Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                      Alignment Scores:
Pred. No.:
Score:
             CTHER INFORMA,
NAME/KEY: CDS
COCATION: (13)
CTHER INFORMA;
NAME/KEY: mod
DCATION: (1)
COTHER INFORMA
US-09-129-112-8
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	ServalvalGlualaalarrpProLeu :::::	; Sequence 1, Application US/09129112; ; Patent No. US20020019995A1; ; GENERAL INFORMATION; ; APPLICANT: Etzler, Marilynn E. ; APPLICANT: The Regents of the University of California ; TITLE OF INVENTION; A No. US20020019995A1 Factor Binding Protein From Legume Roots ; FILE REFERENCE: 023070-079810US ; CURRENT APPLICATION NUMBER: US/09/129,112 ; CURRENT FILING DATE: 1999-08-04 ; PRIOR PILING DATE: 1997-08-06 ; PRIOR FILING DATE: 1997-08-06	NOWINGER OF SEQ 1D NOS: 19 SEQ ID NO SEQ ID NO TYPE: DNA TYPE: DNA NAME/KEY: CDS NOTHER INFORMATION: (51) (1439) NAME/KEY: CDS	US-09-129-112-1 Alignment Scores:	US-09-657-631-4 (1-459) x US-09-129-112-1 (1-1643) QY 3 LysAsnMetGluPheLeulleThrLeullaAlaThrPheLeuLeuLeuMetProAla 22
DB: US-09-657-631-4 (1-459) x US-09-129-112-13 (1-1489) QY 3 LysAsnMetGluPheLeuleThrLeulleAlaThrPheLeuLeuLeuMetProAla 22	. 4 4 4 4	334 GCAGAATCTCTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	514 CAÀTCAGÀTĠCAGTÀTCTTGATGGAACCCAAGAAGGTTCTTATCTTTGGGTGACG 573 181 ValAsnTyrValleuGlyAsnLeuGlyLySSerPerthrLySserValGlyValileAsp 200 181 ValAsnTyrValleuGlyAsnLeuGlyLySSerPerthrLySserValGlyValileAsp 200 181 ValAsnTyrValleuGlyBsrDagarTTTACAAGACAGTGGGGAGTAGTTGAT 633 201 LeuGlyGlyGlyGlyBerValGlnMetThrTyrAlaValSerLySLySThrAlaLySAsnAla 220 201 LeuGlyGlyGlyGlyBerValGlnMetThrTyrAlaValSerLySLySThrAlaLySAsnAla 220 202 LeuGlyGlyGlyGlyGlyGlyGlyGlyAspProTyrIleIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	694 CCAAAGTACTGAAGGAGATCCATACATAAAGAAGCTTGTTACTCCAGGAAAGAAA	281 ThrTyrSerGlyValGluTyrLysAlaPheSerProSerSerGlySerAsnPheAspAsp 300

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Sequence 8688, Application US/10425114

| Sequence 8688, Application No. US20040034888A1
| Publication No. US2004003488BA1
| GENERAL INFORMATION:
| APPLICANT: Liu, Jingdong
| APPLICANT: Abou, Yihua
| APPLICANT: Abou, Yihua
| APPLICANT: Cac, Yongwei
| APPLICANT: Cac, Yongwei
| TILLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
| TILLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
| TILLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
| TILLE OF INVENTION NUMBER: US/10/425,114
| CURRENT FILING DATE: 2003-04-28
| VUMBER OF SEQ ID NOS: 73128
| SEQ ID NO 8688
| LENGTH: 1483
                1382
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AlaValGluAlaIleSerAlaLeuProLysPheLysArgLeuMetTyrPheIle
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Matches:
Conservative:
Mismatches:
Indels:
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1621.50
81.18%
66.74%
68.02%
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Best Local Similarity:
Query Match:
DB:
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US-10-425-114-8688
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                           LysThrProLeuArgLeuGlyAlaThrAlaGlyLeuArgLeuLeuAsnGlyAspAlaAla
                                                                                                                                                                                                        489 GAAAAGATATTGCAAGCGGTTAGGGAAATGTTCAGGAACAGAAGTTCCCTGAGCGTTCAA
                                                                                                                                                                                                                                                                                                          ArgAspAlaValSerIleIleAspGlyThrGlnGluGlySerTyrMetTrpValThrVal
                                                                                                                                                                                                                                                                                                                                                                 AsnTyrValleuGlyAsnLeuGlyLysSerPheThrLysSerValGlyVallleAspLeu
                                                                                                                                                                                                                                                                                                                                                                                    102 LysserLeulleProLeuLeuGluGluAlaGluAspValValProGluAspLeuHisPro
                                                                                                                                                                                                                                                                                                                        ValHisValTyrHisPheAspGlnAsnLeuAspLeuLeuHisIleGlyAsnAspIleGlu
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17 AACATGAATTITCTA-----ACCTICGITACTGITCTACTCTIACTACCAGGAACC
                                                                                                                                                                                                                                                                                                                                               83 ValAspiysIleLysProGlyLeuSerAlaTyrGlyAspAsnProGluGlnAlaAlaLys
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                                                                                                                                                                                                                                                                                                                                                                                                                     63 HisValTyrHisPheAspGlnAsnLeuAspLeuLeuHisIleGlyAsnAspIleGluPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  251 AATAAAAAGATCACACCCGGTTTAAGTGCTTACGAGGATGATCCCGAGCAAGCTGCAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          44 GluThr---LeuThrSerTyrAlaValIlePheAspAlaGlySerThrGlyThrArgVal
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                                                                                                                                                                    Length:
Matches:
Conservative:
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                                                                                                                                                                                                             Mismatches:
Indels:
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-64-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 2234
LENGTH: 1532
                                                                                                                                                                  8.94e-195
1621.50
81.18%
66.74%
68.02%
                                                                                                           ; OTHER INFORMATION: Clone ID: US-10-424-599-2234
                                                                                                                                                                                         Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                US-09-657-631-4 (1-459)
                                                                   TYPE: DNA
ORGANISM: Glycine
                                                                                                                                                   Alignment Scores:
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APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Can Yordwei
APPLICANT: Cao Yordwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
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     AspAlaValSerIleIleAspGlyThrGlnGluGlySerTyrMetTrpValThrValAsn 182
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                    GlyGlySerValGlnMetThrTyrAlaValSerLysLysThrAlaLysAsnAlaProLys
                                                                                                                                                                                                                                            662 CCACCAGAAGAAGAACAAAGATCATAAAAGACTCTTGTACTTAATGGAAAAACTTATGAC
                                                                                                                                                                                                                            LeuTyrvalHisSerTyrLeuArgPheGlyLysGluAlaThrArgAlaGlnValLeuAsn
                                                                                                                                                                                                                                                                                 263 AlaThrAsnGlySerAlaAsnProCysIleLeuProGlyPheAsnGlyThrPheThrTyr
                                                                                                                                                                                                                                                                                                   GlullelleLeuLysValLeuLysValAsnAspProCysProTyrProSerCysThrPhe
                                                          TyrvalLeuGlyAsnLeuGlyLysSerPheThrLysSerValGlyVallleAspLeuGly
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2234, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
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124 TCCTCCGATAATAATTATTCGATTGAAGAACCATTAATGAATCTTATGCAGTTATCTTC 183
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Mismatches:
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Matches:
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Gaps:
            NAME/KEY: primer_bind
LOCATION: (297)...(314)
OTHER INFORMATION: DBX7-for/rev primer
NAME/KEY: primer_bind
LOCATION: (667)...(685)
                                                                                                                                                LOCATION: [688]...(704)
OTHER INFORMATION: DBX2-for/rev primer
NAME/KEY: primer_bind
NAME/CEY: primer_bind
OCATION: Complement ((766)...(785))
OTHER INFORMATION: DBX10 primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ON: (1133)...(1151)
INFORMATION: DBX9-for/rev primer
                                                                      OTHER INFORMATION: DBX1-for/rev primer NAME/KEY: primer bind LOCATION: /FABO. _'....
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OTHER INFORMATION: DBX12 primer
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OTHER INFORMATION: splice site
NAME/KRI: primer_bind
                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: DBX5 primer NAME/KEY: primer bind LOCATION: (933) - (952) OTHER INFORMATION: DBX3 primer NAME/KEY: primer_bind
                                                                                                                                                                                                                                                 NAME/KEY: misc_feature
LOCATIVON: (865)..(857)
OTHER INFORMATION: splice site
NAME/KEY: primer_bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: (955). (972)
OTHER INFORMATION: DBX4 primer
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74.89%
56.44%
58.85%
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LOCATION: (1227)..(12
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Best Local Similarity:
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DB:
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APPLICANT: The Regents of the University of California
TITLE OF INVENTION A No. US20020019995A1 Factor Binding Protein From Legume Roots
TITLE OF INVENTION A NO. US20020019995A1 Factor Binding Protein From Legume Roots
CURRENT APPLICATION NUMBER: US/09/129,112
CURRENT FILING DATE: 1998-08-04
PRIOR PILING DATE: 1997-08-06
RIONER OF SEQ ID NOS: 19
SOFTWARE: Patentin Ver. 2.1
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| TATCAGTATACGTTGCTCGTCGATGGATTTGGCCTGGATCCTTGGAAGAGAGATTATAGTA 1270
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                                                                                                                                                                               PheAlaTyrLeuAlaGluAspValGlyMetValGluProAsnLysProAsnSerIleLeu 362
                                                                        283 SerglyvalGluTyrLygAlaPheSerProSerSerGlySerAsnPheAspAspCysLys 302
                                                                                                850
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                      AlaThrAsnGlySerAlaAsnProCysIleLeuProGlyPheAsnGlyThrPheThrTyr
                                                                                                                                                        GluileileLeulysValleulysValAsnAspProCysProTyrProSerCysThrPhe
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LOCATION: (61)..(1404)
NAME/KEY: primer bind
LOCATION: Complement((1)..(22))
OTHER INPORMATION: DBXtop primer
NAME/KEY: primer bind
LOCATION: (274)..(291)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 18, Application US/09129112; Patent No. US20020019995A1; GENERAL INFORMATION: APPLICANT: Erzler, Marilynn E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Dolichos biflorus
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LOCATION: (1)...(1404)
OTHER INFORMATION: DBX
MAME/KEY: SIG_Peptide
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US-09-129-112-18
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US-10-425-114-11084

i Sequence 11084, Application US/10425114

i Publication No. US20040034888A1

i GENERAL INPORMATION:

APPLICANT: Liu, Jingdong

APPLICANT: Anou, Yihua

APPLICANT: Screen, Steven E

APPLICANT: Screen, Steven E

APPLICANT: Tabaska, Jack E

APPLICANT: Papera, Jack E

APPLICANT: Papera, Jack E

APPLICANT: Papera, Jack E

APPLICANT: Papera, Jack E

APPLICANT: Papera, Jack E

CURRENT PAPEL OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plantes and Uses Thereof for Plant Improvement

CURRENT APPLICATION NUMBER: US/10/425,114

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 73128

SEQ ID NOS: 73128
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                                                       1384 AAATTÁÁTGTÁTTTCCTT 1401
                        454 ArgleuMetTyrPhelle
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GluProAsnLysProAsnSerIleLeuHisProValAspPheGluIleGluAlaLysArg 373
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244 CTTCGCATTGGCCATGACCTTGAGCTGTTCGTCAAGACGAAGCCAGGTTTAAGTGCATAC
                             ArgleuLeuAsnGlyAspAlaAlaGluLysIleLeuGlnAlaThrArgAsnMetPheSer
                                                                                                                                                                                   ValValProGluAspLeuHisProLysThrProLeuArgLeuGlyAlaThrAlaGlyLeu
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GlyLysGlnTyrAspLeuTyrValHisSerTyrLeuArgPheGlyLysGluAlaThrArg 257
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACGGGAAGCCGTGTACATGTCTTTTTAACCAACAATTAGATCTCCTTCGCATTGGC 484
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                                                                                                                                                                                                                                                                                                       GluPheLeuIleThrLeuIleAlaThrPheLeuLeuLeuLeuMetProAlaIleThrSer
                                                                                                                                                                                                                                                                                                                           248 GATTATCTAAATCATACTTTCTCTTTCCAGGTGCTTGCAACTGCAAGTTCTTCT
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  for Plant Improvement
                                                                                                                                                                                                                                                                                US-09-657-631-4 (1-459) x US-10-424-599-87316 (1-1784)
                                                                                                                                                                                                              Conservative:
Mismatches:
Indels:
                                                                                                                                  MRT3847_49857C.
TITLE OF INVENTION: Plants and Uses Thereof: FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 87316
LENGTH: 1784
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Matches:
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1276.00
72.86%
54.91%
53.52%
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                                                                                                TYPE: DNA ORGANISM: Glycine max
                                                                                                                                                                                                                              Best Local Similarity:
Query Match:
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Pred. No.:
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; Sequence 87316, Application US/2040031072A1
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Applicatic David K
; APPLICANT: Cao Yongwei
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
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Fatent No. US20020160378A1

GENERAL INFORMATION:

APPLICANT: Kreps, Joef

APPLICANT: Wang, Xun

APPLICANT: Wang, Xun

APPLICANT: Any Town STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING

TITLE OF INVENTION: SARE, AND METHODS OF USE

TITLE OF INVENTION: SARE, AND METHODS OF USE

TITLE OF INTENTION: SARE, AND METHODS OF USE

FILE REFERENCE: SCRIP1300-3

CURRENT FILING DATE: 2001-08-24

PRIOR PILING DATE: 2001-08-24

PRIOR PLICATION NUMBER: US 60/227,866

PRIOR FILING DATE: 2001-01-16

PRIOR FILING DATE: 2001-01-16

PRIOR FILING DATE: 2001-06-22

NUMBER OF SEQ ID NOS: S379

SEQ ID NO 1888

LENGTH: 1419
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US-09-938-842A-1888
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                               GCTGAGGCTGGATTCGTTGACCCGAAGCAACCTGTTGCTACAGTTCGTCCCATGGACTTT
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                                                                                                                                                     GlulleGluAlaLysArgAlaCysAlaLeuAsnPheGluAspValLysSerThrTyrPro
         GlyGlyGlyGlyGlyGlnLySLySLeupheValThrSerAlaPheAlaTyrLeuAla
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US-09-938-842A-1888
Sequence 1889, Application US/09938842A
Publication No. US20040009476A9
GENERAL INFORMATION:
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                                                                             ArgAsnMetPheSerAsnArgSerThrLeuAsnValGlnArgAspAlaValSerIleIle
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Sequence 849, Application US/09938842A

Patent No. US20020160378A1

GENERAL INFORMATION:

APPLICANT: Harper, Joeff

APPLICANT: Kreps, Joel

APPLICANT: Mang, Xun

APPLICANT: Wang, Xun

APPLICANT: Wang, Xun

APPLICANT: Wang, Xun

APPLICANT: Wang, Xun

APPLICANTON: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING

TITLE OF INVENTION: SAME, AND METHODS OF USE

TITLE OF INVENTION: SAME, AND METHODS OF USE

TITLE OF INVENTION: SAME, AND METHODS OF USE

TITLE OF INVENTION: SAME, AND METHODS OF USE

FILE REPRESENCE: 2001-08-24

PRIOR FILING DATE: 2001-08-24

PRIOR FILING DATE: 2001-01-16

PRIOR FILING DATE: 2001-01-16

PRIOR FILING DATE: 2001-06-22

NUMBER OF SEQ ID NOS: 5379

SEQ ID NOS: 5379
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                                                                    LeuValHisGlyPheGlyLeuGlyProArgLysGluIleThrValGlyGluGlyIleGln 427
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APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Barbazuk, Brad
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5321)B
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NOS: 204966
SEQ ID NOS: 204966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CICAAAGICAAIAAITCAIIGIGIACACACACAIGAAAIGCACITIIGGIGGAGIAIGGAAI 1047
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                                                                               748 TCTTATGTCAGABARTGTATTTGAAGGGACGAAAGTATTTCCTCTATGTTCATAGCTAC
                                                                                                                                                                                    AsnProCysIleLeuProGlyPheAsnGlyThrPheThrTyrSerGlyValGluTyrLys
                                                                                                                                                                                                                                                       289 AlaPheSerProSerSerGlySerAsnPheAspAspCysLysGlullelleLeuLysVal
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ProTyr11eLysLysLeuValLeuLysGlyLysGlnTyrAspLeuTyrValHisSerTyr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCAACTGCAGGTTTGAGAGCTTTGGGTCACCAAGCCTCTGAAAACATTTTGCAAGCGGTT
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GTCATCGAGTACACGATGAAAAACCACGAGGGAGGTTCCAATTCGAGGGGTCCGAAGAAT
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Mismatches:
Indels:
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                 APPLICANT: Rate, con-
APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Wang, Xun
APPLICANT: Alu, Tong
TITLE OF INVENTION: SAME, AND METHODS OF USE
TITLE OF INVENTION: SAME, AND METHODS OF USE
TITLE OF INVENTION: SAME, AND METHODS OF USE
TITLE OF INVENTION: SAME, AND METHODS OF USE
TITLE OF INVENTION: SAME, AND METHODS OF USE
TITLE OF INVENTION: SAME, AND METHODS OF USE
TITLE OF INVENTION: SAME, AND METHODS OF USE
TITLE OF INVENTION: SAME, AND METHODS OF USE
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-6
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 849
                                                                                                                                                                                                                                                                                                                                                                                                    Length:
Matches:
                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Arabidopsis thaliana
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1184.00
70.98%
50.34%
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Best Local Similarity:
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US-09-938-842A-849
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Pred. No.:
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GENERAL INFORMATION:

APPLICANT: Liu, Jingdong

APPLICANT: Liu, Jingdong

APPLICANT: Screen, Steven E

APPLICANT: Screen, Steven E

APPLICANT: Screen, Jack B

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(53313) B

CURRENT APPLICATION NUMBER: US/10/425,114

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 73128

SEQ ID NO 19008
                                                                                                         1335 GTGAAAGCTCTTAAAGTTGACCAAGCATGCACTCACATGAAATGTTCTTTTGGTGGCATT 1394
     1275 AAATTIGAAGCGICGGCTICACCAICIGGIGCIAGITAITCAAAAIGCAGGGAIGAIGIA 1334
                                                                                                                                                                                                                                                                                                                                         1635 ACCTTACTTGTGGATGGATTTGGTGTTGGTTCTCACCAAGAGATGACCTTGGTAAAGAAA 1694
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                                                                                          TrpAsnGlyGlyGlyGlySerGlyGlnLysLysLeuPheValThrSerAlaPheAlaTyr
                                                                                                                                              346 LeuAlaGluAspValGlyMetValGluProAsnLysProAsnSerIleLeuHisProVal
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Matches:
Conservative:
Mismatches:
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; OTHER INFORMATION: Clone ID: LIB3136-007-H10_FLI
US-10-425-114-19008
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Best Local Similarity:
Query Match:
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ORGANISM: Zea mays
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                                                                                                                                                                                                                                                                     30 GlyAsnAsn------LeuLeuThrAsnArgLysIlePheGlnLysGlnGluThrLeu 46
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                                                                                    2071
221
81
123
17
                                                                                 Length:
Matches:
Conservative:
Mismatches:
Indels:
                         OTHER INFORMATION: Clone ID: PAT_MRT4530_34328C.1
                                                                                                                                                                                  US-09-657-631-4 (1-459) x US-10-437-963-29868 (1-2071)
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ORGANISM: Oryza sativa
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APPLICANT: Liu, Jingdong
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APPLICANT: Zhou, Yihua
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ORGANISM: Zea
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